

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 00:33:30 ; Search time 5733.61 Seconds
(without alignments)
10888.092 Million cell updates/sec

Title: US-09-979-558a-1
Perfect score: 1526
Sequence: 1 ttgatcatgctccagatt.....acctggcgctggtacacctc 1526

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
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8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_on.*
21: em_ov.*
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23: em_pat.*
24: em_ph.*
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26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_hgt_hum.*
31: em_hgt_inv.*
32: em_hgt_other.*
33: em_hgt_mus.*
34: em_hgt_pln.*
35: em_hgt_rtd.*
36: em_hgt_rtd.*
37: em_hgt_vrt.*
38: em_sy.*
39: em_hgt_hum.*
40: em_hgt_mus.*
41: em_hgt_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1523	99.8	1526	1	AB016057 Psychroba
2	1523	99.8	1526	6	ES8427 DNA probe f
3	1426.8	93.5	1520	1	AB016059 Psychroba
4	1426.4	93.5	1530	1	AB016058 Psychroba
5	1380.4	90.5	1536	1	AB016054 Psychroba
6	1376.2	90.2	1496	1	AY057116 Psychroba
7	1361.8	89.2	1531	1	AB016055 Psychroba
8	1359.4	89.1	1525	1	AB016056 Psychroba
9	1351.8	88.6	1403	1	AB094456 Psychroba
10	1346.2	88.2	1493	1	AF505746 Gamma pro
11	1333.8	87.4	1485	1	AY167308 Psychroba
12	1328.2	87.0	1476	1	AF505743 Bacterium
13	1327	87.0	1481	1	PG085876 Psychroba
14	1321.4	86.6	1494	1	PSP244766 Psychroba
15	1319.2	86.4	1491	1	PG430828 Psychroba
16	1318.2	86.4	1492	1	PIM30942 Psychroba
17	1316	86.2	1491	1	PJ0430827 Psychroba
18	1315.6	86.2	1515	1	PG131213 Psychroba
19	1312.8	86.0	1491	1	PG1430829 Psychroba
20	1311	85.9	1489	1	AY167286 Psychroba
21	1310.2	85.9	1449	1	AY165583 Unculture
22	1308.2	85.7	1494	1	AF441201 Psychroba
23	1308.2	85.7	1494	1	AF441202 Psychroba
24	1306.6	85.6	1502	1	MP8308373 Marine ps
25	1305.4	85.5	1462	1	PG085877 Psychroba
26	1303.2	85.4	1491	1	PG1430830 Psychroba
27	1302.4	85.3	1451	1	AF005192 Moraxella
28	1302	85.3	1457	1	AF468390 Arctic se
29	1301.2	85.3	1526	1	UBA440989 Antarctic
30	1300	85.2	1462	1	PG085879 Psychroba
31	1299.6	85.2	1469	1	AF260715 Psychroba
32	1298.4	85.1	1463	1	AY167281 Psychroba
33	1298.2	85.1	1445	1	AF468383 Arctic se
34	1298.2	85.1	1488	1	PAF297439 Psychroba
35	1297	85.0	1463	1	AY167301 Psychroba
36	1296.8	85.0	1478	1	PS085875 Psychroba
37	1296.4	85.0	1458	1	PG1539102 Psychroba
38	1296.2	84.9	1496	1	PPA421528 Psychroba
39	1294.6	84.8	1483	1	AF468396 Arctic se
40	1291.2	84.6	1441	1	PG085878 Psychroba
41	1290.4	84.6	1510	1	PSP310992 Psychroba
42	1287.2	84.4	1441	1	AY165598 Unculture
43	1286.8	84.3	1493	1	AF505725 Bacterium
44	1278	83.7	1454	1	AY167289 Psychroba
45	1274.6	83.5	1425	1	AF505739 Bacterium

ALIGNMENTS

RESULT 1
AB016057
LOCUS
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain:NIBH P2K6(T)(=IFO 16279(T)).
ACCESSION AB016057
VERSION AB016057.1 GI:6691638
KEYWORDS 16S ribosomal RNA.
SOURCE Psychrobacter pacificensis
ORGANISM Psychrobacter pacificensis
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE
1 (sites)
AUTHORS Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.
TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan trench, including a description of the deep-sea species
Psychrobacter pacificensis sp. nov
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000).

JOURNAL
MEDLINE
20222194
PUBMED
10758895
REFERENCE
2 (bases 1 to 1526)
Maruyama, A. and Kitamura, K.
Direct Submission
Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
Bioscience and Human-Technology, Department of Applied and
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
Japan (E-mail: maruyama@nibn.go.jp, Tel.: +81-298-54-6062,
Fax: +81-298-54-6412)

FEATURES

Location/Qualifiers
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/mol_type="genomic DNA"
/strain="NIBH P2K6(T)=(IFO 16279(T))"
/db_xref="taxon:112002"
<1..>1526
/product="16S ribosomal RNA"
401 a 332 c 467 g 323 t 3 others

RNA

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTTGATCATGGCTCCAGATTGAAGCACTGGCGGCGAGCTTTACACATCAAGTCGAGCG 60
QY 61 GAACAGATGATAGCTTGTATTAGGGCTGCGAGCNCGGAGGGGTGAGTAATCACTAGGA 120
DB 61 GAACAGATGATAGCTTGTATTAGGGCTGCGAGCNCGGAGGGGTGAGTAATCACTAGGA 120
QY 121 ATCTACTAGTGGGATGAGCTGGGGAACCTCGAATTAATPACCGATGATCTAGC 180
DB 121 ATCTACTAGTGGGATGAGCTGGGGAACCTCGAATTAATPACCGATGATCTAGC 180
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DB 181 GGAGAAAGCAGGGGNTATTAGACTTGGCTATTAGATGAGCCTAAGTCGGATAGCTA 240
QY 241 GATGGTGGGTAAGGCTTACATGGCGAGATCTGTAGCTGGTCTGAGAGGATGATCAG 300
DB 241 GATGGTGGGTAAGGCTTACATGGCGAGATCTGTAGCTGGTCTGAGAGGATGATCAG 300
QY 301 CCACACGGGACTGAGACACGGCCCGGACTCTACGGAGGCGAGCAGTGGGGATATTGGA 360
DB 301 CCACACGGGACTGAGACACGGCCCGGACTCTACGGAGGCGAGCAGTGGGGATATTGGA 360
QY 361 CAATGNGGGAACCCCTGATCCAGCATCCCGCTGTGTGAAGAGGCGCTTTTGGTTGTA 420
DB 361 CAATGNGGGAACCCCTGATCCAGCATCCCGCTGTGTGAAGAGGCGCTTTTGGTTGTA 420
QY 421 AGCATTGAAGCAGTGAAGAGACTCTTGGTTAATACCGGGACCATGACATAGCTG 480
DB 421 AGCATTGAAGCAGTGAAGAGACTCTTGGTTAATACCGGGACCATGACATAGCTG 480
QY 481 CAGAAATAGCAGCGCTAACTCTGTGCCAGCAGCGCGGTAAATACAGAGGGTCAAGCGT 540
DB 481 CAGAAATAGCAGCGCTAACTCTGTGCCAGCAGCGCGGTAAATACAGAGGGTCAAGCGT 540
QY 541 TAATCGGAATTAAGCGGCTAAGCGAGCGTAGGTGGCTGTATAGTCAGATGTAATC 600
DB 541 TAATCGGAATTAAGCGGCTAAGCGAGCGTAGGTGGCTGTATAGTCAGATGTAATC 600
QY 601 CCGGGCTTAACCTGGGACTGCATCTGAACCTGTTAGCTAGAGTGGTGAAGGAGG 660
DB 601 CCGGGCTTAACCTGGGACTGCATCTGAACCTGTTAGCTAGAGTGGTGAAGGAGG 660
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DB 661 TAGAATTCAGGTGTAGCGGTGAATGCGTAGAGATCTGAAGGAATACCGATCGCGAAGG 720
QY 721 CAGCTTCCTGGCATCATACACTGACACTGAGGCTCGAAGCGTGGGTGAGCAACAGGATTAG 780
DB 721 CAGCTTCCTGGCATCATACACTGACACTGAGGCTCGAAGCGTGGGTGAGCAACAGGATTAG 780
QY 781 ATACCTTGGTAGTCCACGCCGTAAAGCATGTCTACTAGTCTGGTGGTTCCTTGGAGACTT 840
DB 781 ATACCTTGGTAGTCCACGCCGTAAAGCATGTCTACTAGTCTGGTGGTTCCTTGGAGACTT 840
QY 841 AGTGAAGCAGCTTAAGCAATTAAGTGAAGCGCTGGGAGTACGGCCGCAAGGTTAAACT 900
DB 841 AGTGAAGCAGCTTAAGCAATTAAGTGAAGCGCTGGGAGTACGGCCGCAAGGTTAAACT 900
QY 901 CAATGAATTAAGTGAAGCGGCCGCGACAGCGGTGGAGCATGTGGTTTAAATTCGATCAACG 960
DB 901 CAATGAATTAAGTGAAGCGGCCGCGACAGCGGTGGAGCATGTGGTTTAAATTCGATCAACG 960
QY 961 CGAAGAACCTTACCTGGTCTTGACATACACAGAAATCTTGTAGAGATACGAGAGTCCCTTC 1020
DB 961 CGAAGAACCTTACCTGGTCTTGACATACACAGAAATCTTGTAGAGATACGAGAGTCCCTTC 1020
QY 1021 GGGAAATGTGATACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 GGGAAATGTGATACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 AAGTCCCGCAAGCGGCAACCCCTTGTCTTGTAGTACAGACTTGGGTGGGAACTCTA 1140
DB 1081 AAGTCCCGCAAGCGGCAACCCCTTGTCTTGTAGTACAGACTTGGGTGGGAACTCTA 1140
QY 1141 AGGATATGCTGCAAGTCAAACTGGAGGAGCGGGAGCGAGCTCAAGTCAATCATGGCCCT 1200
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QY 1201 TACGACAGAGGCTTACACAGCTGCTAATGTTAGTACAGAGGCGAGCTTACAGAGGATG 1260
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QY 1261 TGATGCGAATCTCAAAAGCCCTATCTGCTAGTCCAGATGTTGAGTCTGCAACTCCGACTG 1320
DB 1261 TGATGCGAATCTCAAAAGCCCTATCTGCTAGTCCAGATGTTGAGTCTGCAACTCCGACTG 1320
QY 1321 AAGTAGGAATCGCTAGTAAATCGCGGATCAGAAATCGCGGGTGAATACGTTCCCGGGCCTT 1380
DB 1321 AAGTAGGAATCGCTAGTAAATCGCGGATCAGAAATCGCGGGTGAATACGTTCCCGGGCCTT 1380
QY 1381 GTACACACCGCCCGTCAACACCATGGAGTTGATTGCCAGAGAGTGGTGGTAACTTA 1440
DB 1381 GTACACACCGCCCGTCAACACCATGGAGTTGATTGCCAGAGAGTGGTGGTAACTTA 1440
QY 1441 GTGAGGCGGATCACCGGCTGTGCTGATGACTGGGTGAAGTGGTGAAGTGAAGTGAAGT 1500
DB 1441 GTGAGGCGGATCACCGGCTGTGCTGATGACTGGGTGAAGTGGTGAAGTGAAGTGAAGT 1500
QY 1501 AGGGGAACCTCGCGCTGGATCACCTC 1526
DB 1501 AGGGGAACCTCGCGCTGGATCACCTC 1526

RESULT 2

E58427
LOCUS
DEFINITION
DNA probe for detecting novel psychrophile.
ACCSSION
E58427
VERSION
E58427.1 GI:18622289
KEYWORDS
JP 2000333680-A/1.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 1526)
AUTHORS
Maruyama, A., Kitamura, K. and Kurane, R.
TITLE
DNA probe for detecting novel psychrophile.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 00:33:30 ; Search time 5733.61 Seconds
(without alignments)
10888.092 Million cell updates/sec

Title: US-09-979-558a-1

Perfect score: 1526

Sequence: 1 ttgtgatcgggtccagatt.....acctggcggtggtacacctc 1526

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.fun.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
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- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
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- 30: em.htg_hum.*
- 31: em.htg_inv.*
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- 37: em.htg_vrt.*
- 38: em.sv.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1523	99.8	1526	1	AB016057	AB016057 Psychroba
2	1523	99.8	1526	6	ES8427	ES8427 DNA probe f
3	1426.8	93.5	1520	1	AB016059	AB016059 Psychroba
4	1426.4	93.5	1530	1	AB016058	AB016058 Psychroba
5	1380.4	90.5	1536	1	AB016054	AB016054 Psychroba
6	1376.2	90.2	1496	1	AY057116	AY057116 Psychroba
7	1361.8	89.2	1531	1	AB016055	AB016055 Psychroba
8	1359.4	89.1	1525	1	AB016056	AB016056 Psychroba
9	1351.8	88.6	1403	1	AB094456	AB094456 Psychroba
10	1346.2	88.2	1493	1	AF505746	AF505746 Gamma pro
11	1333.8	87.4	1485	1	AY167308	AY167308 Psychroba
12	1328.2	87.0	1476	1	AF505743	AF505743 Bacterium
13	1327	87.0	1481	1	PG085876	PG085876 Psychroba
14	1321.4	86.6	1494	1	PSE244766	PSE244766 Psychroba
15	1319.2	86.4	1491	1	PGE430828	PGE430828 Psychroba
16	1318.2	86.4	1492	1	PIK309942	PIK309942 Psychroba
17	1316	86.2	1491	1	PJ0430827	PJ0430827 Psychroba
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19	1312.8	86.0	1491	1	PGL430829	PGL430829 Psychroba
20	1311	85.9	1489	1	AY167286	AY167286 Psychroba
21	1310.2	85.9	1449	1	AY165583	AY165583 Unculture
22	1308.2	85.7	1494	1	AF441201	AF441201 Psychroba
23	1308.2	85.7	1494	1	AF441202	AF441202 Psychroba
24	1306.6	85.6	1502	1	MPS308373	MPS308373 Marine ps
25	1305.4	85.5	1462	1	PG085877	PG085877 Psychroba
26	1303.2	85.4	1491	1	PGL430830	PGL430830 Psychroba
27	1302.4	85.3	1451	1	AF005192	AF005192 Moraxella
28	1302	85.3	1457	1	AF468390	AF468390 Arctic se
29	1301.2	85.3	1526	1	PG085879	PG085879 Psychroba
30	1300	85.2	1462	1	PG085879	PG085879 Psychroba
31	1299.6	85.2	1469	1	AF260715	AF260715 Psychroba
32	1298.4	85.1	1463	1	AY167281	AY167281 Psychroba
33	1298.2	85.1	1445	1	AF468383	AF468383 Arctic se
34	1298.2	85.1	1488	1	PAF297439	PAF297439 Psychroba
35	1297	85.0	1463	1	AY167301	AY167301 Psychroba
36	1296.8	85.0	1478	1	PS085875	PS085875 Psychroba
37	1296.4	85.0	1458	1	PGL539102	PGL539102 Psychroba
38	1296.2	84.9	1496	1	PEA421528	PEA421528 Psychroba
39	1294.6	84.8	1483	1	AF468396	AF468396 Arctic se
40	1291.2	84.6	1441	1	PG085878	PG085878 Psychroba
41	1290.4	84.6	1510	1	PSP310992	PSP310992 Psychroba
42	1287.2	84.4	1441	1	AY165598	AY165598 Unculture
43	1286.8	84.3	1493	1	AF505725	AF505725 Bacterium
44	1278	83.7	1454	1	AY167289	AY167289 Psychroba
45	1274.6	83.5	1425	1	AF505739	AF505739 Bacterium

ALIGNMENTS

RESULT 1
LOCUS AB016057 1526 bp DNA linear BCT 10-MAY-2000
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain: NIBH P2K6(T) (=IFO 16279(T)).
ACCESSION AB016057
VERSION AB016057.1 GI:6691638
KEYWORDS 16S ribosomal RNA.
SOURCE Psychrobacter pacificensis
ORGANISM Psychrobacter pacificensis
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE 1 (sites)
AUTHORS Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.
TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan Trench, including a description of the deep-sea species
Psychrobacter pacificensis sp. nov. 835-846 (2000).
 Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000).
 20222194
 MEDLINE
 PUBMED
 REFERENCE
 2 (bases 1 to 1526)
 AUTHORS
 Maruyama, A. and Kitamura, K.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
 Bioscience and Human-Technology, Department of Applied and
 Environmental Microbiology, 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
 Japan (E-mail: maruyama@nib.ac.jp. Tel: +81-298-54-6062,
 Fax: +81-298-54-6412)

FEATURES

source

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/mol_type="genomic DNA"

/strain="NIBH P2K6(T) (=IFO 16279(T))"

/db_xref="taxon:112002"

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/product="16S ribosomal RNA"

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BASE COUNT

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Query Match 99.8%; Score 1523; DB 1; Length 1526;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 301 CCACACGGGACTGAGACACGGCCCGGACTCTAOCGGAGGACGAGTGGGGAATATTGA 360
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 DB 361 CAAATGGGGAACCTGATCCACCATGCGCGTGTGAGAGAGGCGCTTTGGTGTAA 420
 QY 421 AGCACTTTAAGCAGTGAAGAGACTCTCGGTTAATACCCGGGACGATGACATTAGCTG 480
 DB 421 AGCACTTTAAGCAGTGAAGAGACTCTCGGTTAATACCCGGGACGATGACATTAGCTG 480
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 DB 541 TAATCGGAATTAAGCGGCTAAGCGGCTAGGTGGCTTGTATAGTCAGATGTAATC 600
 QY 601 CCGGGCTTAACCTGGGAATCTGATCTGAACTGTAGCTAGATAGGTGAGGGAAG 660
 DB 601 CCGGGCTTAACCTGGGAATCTGATCTGAACTGTAGCTAGATAGGTGAGGGAAG 660
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DB 661 TAGAATTCAGGTGTAGCGTGAATCGGTAGATCTGAGGAATACCGATGGCGAAG 720
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 DB 721 CAGCTTCCTGGCATCACTACTAGTACTGAGGCTCGAAGAGCTGGGTAGCAACAGATTAG 780
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 DB 781 ATACCTTGGTGGTCCAGCGGCTTAACGATGCTACTAGTCTGTTGGTCCCTGAGGACTT 840
 QY 841 AGTGACGAGCTTAACGCAATAAGTAGACCGCTGGGAGTAGCGCGCAAGGTAAACT 900
 DB 841 AGTGACGAGCTTAACGCAATAAGTAGACCGCTGGGAGTAGCGCGCAAGGTAAACT 900
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 DB 901 CAAATGAATTCAGCGGGGCGCGCACAGCGGTGAGCATGTGGTTAATTCATGCAACG 960
 QY 961 CGAAGAACCTTACCTGCTTGCATACACAGAACTCTGTAGAGATACGAGAGTGCCTTC 1020
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 DB 1081 AGTCCCGACAGGACGCAACCTTGTCTTAGTACCAGCACTTCGGTGGGAATCTTA 1140
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RESULT 2

E58427

LOCUS

E58427 1526 bp DNA linear PAT 31-JAN-2002

DEFINITION DNA probe for detecting novel psychrophile.

ACCESSION

E58427

VERSION

E58427.1 GI:18622289

KEYWORDS

JP 2000333680-A/1.

SOURCE

unidentified

ORGANISM

unclassified

REFERENCE

1 (bases 1 to 1526)

AUTHORS

Maruyama, A., Kitamura, K. and Kurane, R.

TITLE

DNA probe for detecting novel psychrophile

JOURNAL

Patent: JP 2000333680-A 1 05-DEC-2000;

AGENCY OF IND. SCIENCE & TECHNOL

OS Psychrobacter pacificus

PN JP 2000333680-A/1

PD 05-DEC-2000

PF 25-MAY-1999 JP 1999145342

PR

PI AKIHIKO MARYAMA, KEIKO KITAMURA, RYUICHIRO KURANE PC

C12N15/09, C12N1/20, C12Q1/68//C12N15/09, C12R1/01, (C12N1/20, PC

C12R1/01),

PC C12N15/00, (C12N15/00, C12R1/01)

CC

FH Key Location/Qualifiers

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Matches 1526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ATCTACTAGTAGTGGGGATAGCTCGGGGAACTCGAATTAATACCGCATACGCTCTACG 180

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QY 361 CAATGNGGGAACCTGTATCCAGCATCGCGCTGTGTGAAGAAGCGCTTTTGGTTGTA 420

DB 361 CAATGNGGGAACCTGTATCCAGCATCGCGCTGTGTGAAGAAGCGCTTTTGGTTGTA 420

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QY 1501 AGGGGAACCTTCGGCTGGATCACCTC 1526

DB 1501 AGGGGAACCTTCGGCTGGATCACCTC 1526

RESULT 3

AB016059

LOCUS

DEFINITION

Psychrobacter pacificus strain: NIBH P2K18.

ACCESSION

AB016059

VERSION

AB016059.1 GI:6691640

KEYWORDS

16S ribosomal RNA.

SOURCE

Psychrobacter pacificus

ORGANISM

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.

REFERENCE

1 (sites)

AUTHORS

Muryama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.

TITLE

Phylogenetic analysis of psychrophilic bacteria isolated from the

AB016059 1520 bp DNA linear BCT 10-MAY-2000
Psychrobacter pacificus strain: NIBH P2K18.

AB016059 GI:6691640

AB016059.1 16S ribosomal RNA.

Psychrobacter pacificus

Psychrobacter pacificus

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Moraxellaceae; Psychrobacter.

1 (sites)

Muryama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.

Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan Trench, including a description of the deep-sea species
 Psychrobacter pacificensis sp. nov
 Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
 20222194
 10758895
 2 (bases 1 to 1520)
 Maruyama, A. and Kitamura, K.
 Direct Submission
 Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
 Bioscience and Human-Technology, Department of Applied and
 Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
 Japan [E-mail: maruyama@nibh.go.jp, Tel:+81-298-54-6062,
 Fax:+81-298-54-6412]

FEATURES

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 /db_xref="taxon:112002"
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BASE COUNT 398 a 332 c 467 g 322 t 1 others
 ORIGIN

rRNA

Query Match 93.5%; Score 1426.8; DB 1; Length 1520;
 Best Local Similarity 98.8%; Pred. No. 0;
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RESULT 4

AB016058

LOCUS
 DEFINITION

Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
 strain:NIBH P2K17.

AB016058

ACCESSION

VERSION

AB016058.1 GI:6691639

KEYWORDS

16S ribosomal RNA.

SOURCE

Psychrobacter pacificensis

Psychrobacter pacificensis

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Moraxellaceae; Psychrobacter.

REFERENCE

1 (sites)

Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.

Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan Trench, including a description of the deep-sea species

Psychrobacter pacificensis sp. nov

JOURNAL Int. J. Syst. Evol. Microbiol., 50 Pt 2, 835-846 (2000)
 MEDLINE 20222194
 PUBMED 10758895
 REFERENCE 2 (bases 1 to 1530)
 AUTHORS Maruyama, A. and Kitamura, K.
 TITLE Direct Submission
 JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
 Bioscience and Human Technology, Department of Applied and
 Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
 Japan (E-mail: maruyama@nibh.go.jp, Tel.: +81-298-54-6062,
 Fax: +81-298-54-6412)

FEATURES
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RESULT 5
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 strain:NIBH P2J2.
 DEFINITION
 AB016054
 ACCESSION
 AB016054.1 GI:6691635
 VERSION
 16S ribosomal RNA.
 KEYWORDS
 Psychrobacter pacificensis
 SOURCE
 Psychrobacter pacificensis
 ORGANISM
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Moraxellaceae; Psychrobacter.
 REFERENCE
 1 (sites)
 AUTHORS Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.
 TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the
 Japan Trench, including a description of the deep-sea species
 psychrobacter pacificensis sp. nov
 JOURNAL Int. J. Syst. Evol. Microbiol., 50 Pt 2, 835-846 (2000)
 MEDLINE 20222194

King's College London, Guy's Hospital, London SE1 9RT, United Kingdom
 Direct Submission
 3 (bases 1 to 1496)
 Zandvliet,D., Coleman,D. and Coates,A.
 Direct Submission
 Submitted (25-SEP-2001) Medical Microbiology, St George's Hospital
 Medical School, Cranmer Terrace, London SW17 0RE, United Kingdom
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 QY 568 CGCTAGTGTGCTTGAATAGTCAAGTGAATCCCGGGCTTAACCTGGGACGTGATCT 627
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 QY 628 GAACTGTAGGCTAGTGTGAGAGGGAAGTAGAATTCAGGTGTAGCGGTGAATG 687
 Db 610 GAATCTGTGCTAGTGTGAGAGGGAAGTAGAATTCAGGTGTAGCGGTGAATG 669
 QY 688 GCTAGAGATCTGAAGGAATACCGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 747
 Db 670 GCTAGAGATCTGAAGGAATACCGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 729

QY 748 AGCTCGAAAGCGTGGGTAGCAACACAGGATTAGATACCTGTGTAGTCCACGCGCTAAACG 807
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 Db 850 CGCTCGGGAGTACGCGCGCAAGGTTAAACTCAATGAATGAGCGGGGCGCCGACAA 909
 QY 928 CGCTGGAGCATGTGTTTAAATTCGATCAACGCGAAGACCTTACCTGGTCTTGACATA 987
 Db 910 CGCTGGAGCATGTGTTTAAATTCGATCAACGCGAAGACCTTACCTGGTCTTGACATA 969
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 Db 970 CACAGAATCTTGTAGAGATACGAGAGTCCCTTCGGGAAATTTGTATACAGGTGCTCATGG 1029
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 Db 1030 CTGCTGTCAGTCTGTGTGAGATGTTGGTTTAAAGTCCCGCAACGAGCGCAACCTTGT 1089
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 Db 1090 CTTTAGTTACAGCACTTCGGGTGGAACTCTAAGGATCTGCCAGTGAACAACCTGGAGG 1149
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 Db 1449 ATGCTGGGTGAAGTCTGTAACAAGGTAGCGGTAGGGGAACCTGCGGC 1496

RESULT 7
 LOCUS AB016055 1531 bp DNA linear BCT 10-MAY-2000
 DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
 strain:NTBH P2J3.
 ACCESSION AB016055
 VERSION AB016055.1 GI:6691636
 KEYWORDS 16S ribosomal RNA
 SOURCE Psychrobacter pacificensis
 ORGANISM Psychrobacter pacificensis
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Moraxellaceae; Psychrobacter.
 REFERENCE 1 (sites)
 AUTHORS Maruyama A., Honda D., Yamamoto H., Kitamura K. and Higashihara T.
 TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the
 Japan Trench, including a description of the deep-sea species
 Psychrobacter pacificensis sp. nov
 JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
 MEDLINE 20222194
 PUBMED 10758895

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1496	GCCGTAGGGGAACCTCGCGCTGGATCACCT	1525
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RESULT 8	AB016056	
LOCUS	AB016056	
DEFINITION	Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain: NIEB P2U13.	
ACCESSION	AB016056	
VERSION	AB016056.1	GI:6691637
KEYWORDS	16S ribosomal RNA.	
SOURCE	Psychrobacter pacificensis	
ORGANISM	Psychrobacter pacificensis	
REFERENCE	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.	
AUTHORS	1 (sites)	
TITLE	Murayama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.	
JOURNAL	Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species Psychrobacter pacificensis sp. nov	
MEDLINE	Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)	
PUBLISHED	2022194	
REFERENCE	10758895	
AUTHORS	2 (bases 1 to 1525)	
	Murayama, A. and Kitamura, K.	

TITLE Direct Submission
JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of Bioscience and Human-Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062, Fax:+81-298-54-6412)

FEATURES Location/Qualifiers
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/strain="NIBH P2J13"
/db_xref="taxon:112002"
c1. >1525
/product="16S ribosomal RNA"
BASE COUNT 398 a 334 c 468 g 325 t
ORIGIN

Query Match 89.1%; Score 1359.4; DB 1; Length 1525;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1456; Conservative 0; Mismatches 34; Indels 8; Gaps 7;

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RESULT 9
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LOCUS 1403 bp DNA linear BCT 16-JAN-2003
DEFINITION Psychrobacter sp. MJVP.15.12 gene for 16S rRNA, partial sequence.
ACCESSION AB094456
VERSION AB094456.1 GI:27807566
KEYWORDS
SOURCE
ORGANISM
Psychrobacter sp. MJVP.15.12
Psychrobacter sp. MJVP.15.12
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
1
Inagaki, F., Suzuki, M., Takai, K. and Horikoshi, K.
Microbial community structure in subseafloor sediments from the Sea
of Okhotsk
Published Only in Database (2003)
REFERENCE
2 (bases 1 to 1403)
JOURNAL
AUTHORS
TITLE
DIRECT SUBMISSION
Inagaki, F.
Submitted (23-OCT-2002) Fumio Inagaki, Japan Marine Science &
Technology Center, Subground Animalcule Retrieval (SUGAR) Project,
Frontier Research System for Extremophiles; Natsuchina-cho 2-15,
Yokosuka 237-0061, Japan (E-mail:inagaki@jamstec.go.jp,
Tel:81-468-67-9687, Fax:81-468-67-9715)

FEATURES		Location/Qualifiers	
source	1..1403	/organism="Psychrobacter sp. MJYP.15.12"	
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Best Local Similarity	99.4%; Pred. No. 0;		
Matches 1386; Conservative	0; Mismatches 5; Indels 3; Gaps 3;		
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QY	90	GAGCNGCCGAGCGGTGAGTAATCTAGGAATCTACCTAGTCTAGTGGGGATAGCTCGGS	149
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QY	150	GAACCTCGAATTAATACCGCATAGCT-CTACGGGAGAAAGCAGGGGNTCAATTAGACCTTG	208
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QY	209	CGCTATTAGATGAGCTTAAGTCGGATAGCTAGATGTTGGGGTAAAGGCTACCATGGCG	268
Db	190	CGCTATTAGATGAGCTTAAGTCGGATAGCTAGATGTTGGGGTAAAGGCTACCATGGCG	249
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QY	329	CT-CTACGGGAGGACGAGTGGGAAATATTGGACAATGNGGGAAACCCCTGATCCAGCCAT	387
Db	310	CTCCTACGGGAGGACGAGTGGGAAATATTGGACAATGNGGGAAACCCCTGATCCAGCCAT	369
QY	388	GGCGGCTGTGTGAAGAAGGCTTTTGGTGTGAAGCACTTTAAGCAGTGAAGAGACTCT	447
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QY	448	TCGGTTAATACCCGGGAGGATGACATTAGCTGCAGAAATAGCACCGCGCTAACTCTGTGC	507
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QY	988	CACAGAACTTGTAGAGATACGAGAGTCCCTTCGCGGAATTTGTATACAGGTCTCATGG	1047
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QY	1168	AAGCGGGGAGCAGCTCAAGTCTCATGTCCTTACGACAGGCTACACAGCTGTCTACA	1227
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QY	1288	AGTCCAGATGAGTCTGCAACTCGACTCCATGAAGTAGGATCGCTAGTAATCGCGGAT	1347
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QY	1348	CAGAACTCCCGGCTGAATPACTTCCCGGGCTTGTACACACCGCCCTCACACATGGGA	1407
Db	1330	CAGAACTCCCGGCTGAATPACTTCCCGGGCTTGTACACACCGCCCTCACACATGGGA	1389
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Db	1390	GTTGATTGCACAG 1403	
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LOCUS	Gamma proteobacterium UMB21A 16S ribosomal RNA gene, partial		
DEFINITION	sequence.		
ACCESSION	AF505746		
VERSION	AF505746.1	GI:28173023	
KEYWORDS	gamma proteobacterium UMB21A		
SOURCE	Bacteria; Proteobacteria; Gammaproteobacteria.		
ORGANISM	Tang,R.J. and Cooney,J.J.		
REFERENCE	1 (bases 1 to 1493)		
AUTHORS	Tributylin-resistant, biofilm-forming bacteria isolated from		
TITLE	Boston Harbor, MA		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1493)		
AUTHORS	Tang,R.J. and Cooney,J.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-APR-2002) Environmental, Coastal and Ocean Sciences,		
	University of Massachusetts Boston, 100 Morrissey Blvd., Boston, MA		
	02125-3393, USA		
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 partial sequence.
 AY167308
 AY167308.1 GI:28624950
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 PSYCHROBACTER GLACINCOLA
 Psychrobacter glacincola
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Moraxellaceae; Psychrobacter.
 1 (bases 1 to 1485)
 Brinkmeyer, R., Knittel, K., Juergens, J., Weyland, H., Amann, R. and
 Helmke, E.
 Diversity and Structure of Bacterial Communities in Arctic versus
 Antarctic Sea Ice: A Comparison
 Unpublished
 2 (bases 1 to 1485)
 Brinkmeyer, R., Knittel, K., Juergens, J., Weyland, H., Amann, R. and
 Helmke, E.
 Direct Submission
 Submitted (21-OCT-2002) Alfred Wegener Institute for Polar and
 Marine Research, Am Handelsshafen 12, Bremerhaven D-27570, Germany
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 BASE COUNT
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Query Match	87.4%; Score 1333.8; DB 1; Length 1485;
Best Local Similarity	95.9%; Pred. No. 0;
Matches 1420; Conservative	0; Mismatches 55; Indels 5; Gaps 5;
QY	30 GCGCGGAGGCTTTACACATCAAGTCGACGCGAAGACGATAGCTGTCTATTAGCGCTC 89
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QY	90 GAGCNGCGGAGCGGGTGAATTAAGTAATCTACCTAGTGTAGTGGGGATAGCTCGG 149
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QY	150 GAACCTCGAATTAATACCGCATACCTCTACGGGGAAGACAGGGGTCATTAGACTTGC 209
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SOURCE	bacterium UMB13F
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TITLE	Tributyltin-resistant, biofilm-forming bacteria isolated from Boston Harbor, MA
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1476)
AUTHORS	Tang,R.J. and Cooney,J.J.
TITLE	Direct Submission
JOURNAL	Submitted (23-APR-2002) Environmental, Coastal and Ocean Sciences, University of Massachusetts Boston, 100 Morrissey Blvd., Boston, MA 02125-3393, USA
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LOCUS
DEFINITION
ACCESSION
VERSION
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SOURCE
ORGANISM

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AJ244766.1 GI:22217963
16S ribosomal RNA; 16S rRNA gene.
Psychrobacter sp. V4.BO.14
Psychrobacter sp. V4.BO.14
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.

REFERENCE
AUTHORS
TITLE

Fritz,I.
Das Bakterioplankton im Westlichen Mittelmeer. Analyse der
taxonomischen Struktur freilebender und partikelgebundener
bakterieller Lebensgemeinschaften mit mikrobiologischen und
molekularbiologischen Methoden
Thesis (2000) Gemeinsame Naturwissenschaftliche Fakultät,
Technische Universität Carolo-Wilhelmina Braunschweig,
Braunschweig, GERMANY
http://www.biblio.tu-bs.de/ediss/data/2000081la/2000081la.html
2 (bases 1 to 1494)
Fritz,I.
Direct Submission

JOURNAL
Submitted (28-APR-1999) Fritz I., Dept. Microbiology - Microbial
Ecology Workgroup, GBF - National Research Center for
Biotechnology, Mascheroder Weg 1, Braunschweig, Lower Saxony 38124,
Germany
revised by author

REMARK
FEATURES
source

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1158	75.9	1535	20	AAX83569	16S rDNA gene frag
5	1153.2	75.6	1528	20	AAX83570	16S rDNA gene frag
6	1153.2	75.6	1535	20	AAX83571	16S rDNA gene frag
7	1129.2	74.0	1535	20	AAX83568	16S rDNA gene frag
8	1121.4	73.5	1529	20	AAX83564	16S rDNA gene frag

ALIGNMENTS

RESULT 1	
AAC87531	
ID	AAC87531 standard; DNA; 1526 BP.
XX	AC
XX	AAC87531;
XX	
XX	13-MAR-2001 (first entry)
XX	
DE	Psychrobacter pacificensis NIBH P2K6 16S rDNA, SEQ ID NO:1.
XX	
XX	16S rDNA; species-specific detection; identification;
KW	psychrophilic bacterium; oceanic circulation; Psychrobacter;
KW	strain NIBH P2K6; ds.
XX	
OS	Psychrobacter pacificensis.
XX	
PN	WO200071705-A1.
XX	
PD	30-NOV-2000.
XX	
XX	25-MAY-2000; 2000WO-JP03372.
XX	
PR	25-MAY-1999; 99JP-0145342.
PR	30-MAR-2000; 2000WO-JP02045.
XX	
XX	(AGEN) AGENCY OF IND SCI & TECHNOLOGY.
XX	
PI	Maruyama A, Kitamura K, Kurane R;
XX	
DR	WPI; 2001-025158/03.
XX	

16S rDNA gene frag
16S rDNA gene frag
16S rDNA gene frag
Polyhydroxyalkanol
Polyhydroxyalkanol
Pseudomonas jessen
Pseudomonas jessen
Pseudomonas jessen
Pseudomonas jessen
Pseudomonas jessen
Nucleotide sequenc
Pseudomonas jessen
16S ribosomal RNA
Cyclocloasticus pug
Aliphatic hydrocar
Benzene-degrading
Benzene-degrading
E. coli 16S riboso
Pseudomonas aerugi
E. coli MG1655 rrn
Escherichia coli 1
Escherichia coli 1
rRNA gene (rrsE) f
E. coli 16S rRNA.
Escherichia coli r
Escherichia coli i
Klebsiella pneumon
E. coli 16S rRNA s
E. coli MG1655 rrn
Cyclocloasticus pug
E. coli MG1655 rrn
E. coli MG1655 rrn
E. coli MG1655 rrn
Salmonella typhimu
Cyclocloasticus pug
Escherichia coli i
E. coli 16S rRNA f
E. coli MG1655 rrn
E. coli MG1655 rrn

RESULT 3

AAQ13256

ID AAQ13256 standard; DNA; 1485 BP.

XX AC AAQ13256;

XX 25-MAR-2003 (updated)

DT 25-OCT-1991 (first entry)

XX DE 16S rRNA gene (partial).

XX Probe; detection; Moraxella; Neisseria; 23S; ribosomal RNA; ss.

XX OS Branhameilla catarrhalis ITG 4197.

XX PN WO9111531-A.

XX PD 08-AUG-1991.

XX PF 01-FEB-1991; 91WO-EP00211.

XX PR 02-FEB-1990; 90EP-0400297.

XX PA (INNO-) INNOGENETICS NV SA.

XX PI Rossau R, Vanheuers H;

XX DR WPI; 1991-252662/34.

XX PT Nucleic acid probes for selective detection of Branhameilla

XX PT catarrhalis - can detect bacterial RNA or DNA and differentiate

XX PT it from other bacteria

XX PS Disclosure; Fig 1(A); 4lpp; English.

XX CC This sequence was used to derive the probes BCI-BC5 as represented

XX CC in AAQ13258-67. Probes BC9 as represented in AAQ13268-69 are derived

XX CC from the 23S rRNA gene (AAQ13257).

XX CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 1485 BP; 390 A; 325 C; 449 G; 320 T; 1 other;

Query Match 78.3%; Score 1195; DB 12; Length 1485;

Best Local Similarity 90.6%; Pred. No. 0;

Matches 1352; Conservative 0; Mismatches 128; Indels 12; Gaps 7;

QY 36 AGCGTTAACACATGCAAGTGCAGCGGAAACGATGATGCTTCTTATAGCGTCGAGCNG 95

DB 1 AGCGTTAACACATGCAAGTGCAGCGGAAACGATGATGCTTCTTATAGCGTCGAGCNG 56

QY 96 CCGGACGGGTGAGTAACTTAGCAATCTAGTCTAGTGGGATAGCTCGGGAACT 155

DB 57 GCGGACGGGTGAGTAACTTAGCAATCTAGTCTAGTGGGATAGCTCGGGAACT 116

QY 156 CGAATTAATACCGCATAGCTCTAGCGGAAAGAGGAGGNTCATTAGACCTTCGGCTATT 215

DB 117 CAAGCTTAATACCGCATAGCTCTAGCGGAAAGAGGAGGNTCATTAGACCTTCGGCTATT 172

QY 216 AGATGAGCCTAAGTCGGATTAGCTAGTGGGTAAAGCCCTACCATGGGACGATCT 275

DB 173 AGATGAGCCTAAGTCGGATTAGCTAGTGGGTAAAGCCCTACCATGGGACGATCT 232

QY 276 GTAGCTGGTCTGAGAGGATGATACGACACCGGACTGAGACGCGCCGGACT-CTAC 334

DB 233 GTAGCTGGTCTGAGAGGATGATACGACACCGGACTGAGACGCGCCGGACTCTAC 292

QY 335 GGGAGGCACAGTGGGGATATTGGCAATGNGGGAACCCCTGATCCAGCCATGCCGGCT 394

DB 293 GGGAGGCACAGTGGGGATATTGGCAATGNGGGAACCCCTGATCCAGCCATGCCGGCT 352

QY 395 GTGTGAAGAGGCCCTTTGGTTGTAAGACACTTAAAGCACTTAAAGCACTTTCGGTTA 454

DB 353 GTGTGAAGAGGCCCTTTGGTTGTAAGACACTTAAAGTGGGAGGAACCTTATGGTTA 412
 QY 455 ATACCCGGGACGATGACATTAGCTGCAGAAATAAGCACCGGCTAACTCTGTGCCAGCAGC 514
 DB 413 ATACCCATAAGCCCTGAGCTTACCCACAGAAATAAGCACCGGCTAACTCTGTGCCAGCAGC 472
 QY 515 CCGGCTAATACAGAGGCTGCAAGCGTTAATCGGAATTAATCGGGCTAAAGCAGCGGTAGG 574
 DB 473 CCGGCTAATACAGAGGCTGCAAGCGTTAATCGG-ATTACTGGGCTAAAGCAGCGGTAGG 531
 QY 575 TGGCTTGATAAGTCAGATGTAATCCCGGCTTAACCTGGGAACGATCATCTGAAACTG 634
 DB 532 TGGTTTATTTAGTCAGATGTAAGCCCGGCTTAACCTGGGAACGATCATCTGACTCTG 591
 QY 635 TTAGGCTAGAGTGGTGGAGGAAAGTAAATTTAGGTGTAGCGGTGAAATGCGGTAGAG 694
 DB 592 GATACTAGAGTGGTGGAGGGGNGTAGAATTCAGGTGTAGCGGTGAAATGCGGTAGAG 651
 QY 695 ATCTGAAGCAATACCGATGCGGAGGAGCGAGCTTCTGGCATCATCTGACTGAGGCTCG 754
 DB 652 ATCTGGAGCAATACCGATGCGGAGGAGCGAGCTTCTGGCATCATCTGACTGAGGCTCG 711
 QY 755 AAAGCGTGGGTAGCAACACAGGATTTAGATACCTGTGTAGTCCACGCCGTAAACGATGCTTA 814
 DB 712 AAAGCGTGGGTAGCAACACAGGATTTAGATACCTGTGTAGTCCACGCCGTAAACGATGCTTA 771
 QY 815 CTAGCTGTTGGTCCCTTGGAGACTTAGTGCACGAGCTTAACGCAATAAGTAGACGCCCTG 874
 DB 772 CCAGTGGTGGTCTTTTAAAGACTTAGTGCACGAGTTAAACGCAATAAGTAGACGCCCTG 831
 QY 875 GGAGTACCGGCGCAAGGTAAACATCAATGAATTTAGCGGGGCCCGGCACAGCGGTGG 934
 DB 832 GGAGTACCGGCGCAAGGTAAACATCAATGAATTTAGCGGGGCCCGGCACAGCGGTGG 891
 QY 935 AGCATGTGTTTAAATTCGATGCAACGCAAGAACCTTACCTGGTCTTTGACATACACAGAA 994
 DB 892 ASCATGTGTTTAAATTCGATGCAACGCAAGAACCTTACCTGGTCTTTGACATAGTAGAA 951
 QY 995 TCTTTAGAGATACGAGAGTGCCTTCGGGAATTTGATGATACAGGTGCTGATGCTGTGCT 1054
 DB 952 TCTTGCAGAGATGCGAGAGTGCCTTCGGGAATTTGATGATACAGGTGCTGATGCTGTGCT 1011
 QY 1055 CAGCTGCTGCTGAGATGTTGGTTAAAGTCCGCAAGCGAGCAACCTTTGCTCTTACT 1114
 DB 1012 CAGCTGCTGCTGAGATGTTGGTTAAAGTCCGCAAGCGAGCAACCTTTTCTTACT 1071
 QY 1115 TACACGACTTCCGTTGGGAACTCTAAGGATATCTCCAGTGCACAACTGGAGGAGCGG 1174
 DB 1072 TACACGACTTCCGTTGGGAACTCTAAGGATATCTCCAGTGCACAACTGGAGGAGCGG 1131
 QY 1175 GGAGGAGCTCAAGTCAATCATGCGCCCTTACGACCGGCTACACAGTGTACATGATGAT 1234
 DB 1132 GGAGGAGCTCAAGTCAATCATGCGCCCTTACGACCGGCTACACAGTGTACATGATGAT 1191
 QY 1235 GTACAGAGGAGCTCACACAGGATGTGATGGAATCTCAAAAAGCCCTATCTGATGCTAG 1294
 DB 1192 GTACAAAGGTTGCTACACAGGATGTGATGCTAATCTCAAAAAGCCCTATCTGATGCTAG 1251
 QY 1295 ATTGGAGTCTGCAACTGCACTGCATGATGATGATGATGATGATGATGATGATGATGATG 1354
 DB 1252 ATTGGAGTCTGCAACTGCACTGCATGATGATGATGATGATGATGATGATGATGATGATG 1311
 QY 1355 CCGCGTGAATACGTTCCCGGCTTGTACACACCGCCCTCACACCATCGGAGTGTGAT 1414
 DB 1312 CTCGGTGAATACGTTCCCGGCTTGTACACACCGCCCTCACACCATCGGAGTGTGAT 1371
 QY 1415 GCACCAAGAGTGTGATGCTTAACTTAGTGGAGGCGGATCACACCGTGTGTGATGATG 1474
 DB 1372 TCACCAAGAGTGTGATGCTTAACTTAGTGGAGGCGGATCACACCGTGTGTGATGATG 1430
 QY 1475 GGTGAGTGTGATGCTTAACTTAGTGGAGGCGGATCACACCGTGTGTGATGATGATG 1526

Db 1431 GGGTGAAGTCGTAACAAGTAGTCGGTAGGGAA-CTGGGCTGGATCACCTC 1481

RESULT 4
AAX83569
ID AAX83569 standard; DNA; 1535 BP.
XX
XX AAX83569;
AC AAX83569;
XX 21-DEC-1999 (first entry)
DT
XX
DE 16S rDNA gene fragment from marine bacterium, isolate K3-3.
XX
XX Monitoring; oil; contamination; sea water; detection; flagellum;
KW Gram-negative bacterium; Proteobacteria; glucose; carbon source;
KW alkane; 16S rDNA gene; ds.
XX
XX Proteobacteria.
OS
XX
XX JP11243967-A.
PN
XX
XX 14-SEP-1999.
PD
XX
XX 04-MAR-1998; 98JP-0069399.
PF
XX
XX 04-MAR-1998; 98JP-0069399.
PR
XX
XX (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
PA
XX
XX WPI; 1999-564435/48.
DR
XX
XX Monitoring of oil contamination of sea water - where oil contamination
PT is evaluated by detection of a microbe having properties from e.g.
PT having no flagellum, being a Gram-negative bacterium, belonging to
PT Proteobacteria, gamma subdivision, etc.2
XX
XX Claim 3; Page 7-8; 15pp; Japanese.
PS
XX
XX The invention relates to a method for monitoring oil contamination of
CC sea water by detecting, in the sea water, a microbe having the following
CC properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium;
CC (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot
CC assimilate glucose as a single carbon source; and (5) it efficiently
CC assimilates at least one of 10-30C n-alkanes. This sequence represents
CC a fragment of the 16S rDNA gene from the microbe of the invention,
CC isolate K3-3.
XX
XX Sequence 1535 BP; 375 A; 350 C; 496 G; 314 T; 0 other;
SQ

Query Match 75.9%; Score 1158; DB 20; Length 1535;
Best Local Similarity 87.8%; Pred. No. 0;
Matches 1318; Conservative 0; Mismatches 178; Indels 5; Gaps 5;

QY 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATCAGTTCCTATTAGGCGTC 89
Db 32 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATGTTCTTACCAGCGCTC 91
QY 90 GAGCNGCCGACGCGGTGAGTAATCTTAGGAATCTACCTAGTAGTGGGGATAGCTCGGG 149
Db 92 GAGCGG-CGAGCGGCTGAGTACCGCGTGAGATCTGCCATTTGTGGGGATACCTTGGG 150
QY 150 GAACACTCGAATTAATACCCAT-ACGTTCTACGGGAGAAACGAGCGGNTCAATTAGACCTTG 208
Db 151 GAACACTCAAGCTAATACCCATATPCCCTACGGGGGAAACGAGCGGACCTTCGGGCGCTTG 210
QY 209 CGCTATTAGATGAGCCTAATGCGGATAGCTAGATGGTGGGTAAGCCCTACCATGGCG 268
Db 211 TGCAGATGGATGAGCTTCGCGCTCGGATGATGATGTTGGTGAAGGCCCTACCAAGGCG 270
QY 269 ACGATCTGATGCTGCTGAGAGGATGATCAGCCACACCGGACCTGACACACGCGCGGA 328
Db 271 ACGATCGTACGTGGTCTGAGAGGATGATCAGCCACACCGGACCTGACACACGCGCGGA 330

QY 329 CT-CTACGGGSGCAGCAGTGGGGAATATTGGCAATATGNGGSGAAACCCCTGATCCAGCCAT 387
Db 331 CTCCTACGGGAGCAGCAGTGGGGAATCTTGGCAATATGNGGSGAAACCCCTGATCCAGCCAT 390
QY 388 GCGCGCTGTGTGAAGAAGCCCTTTTGGTTGTTAAAGCACTTTTAAGCAGTGAGAGACTCT 447
Db 391 GCGCGTGTGTGAAGAAGCCCTTAGGGTTGTTAAAGCACTTTTCAGCAGGAGGAGGCTTC 450
QY 448 TCGGTTAATACCCGGGAGCGATGACATAGCTCAGAAATAGCACCAGGCTTAATCTGTGC 507
Db 451 GAGTTAATACCTTGGAGTACTTGAGTTAGCTCAGAGAAGACCCGCTAATTTCTGTCG 510
QY 508 CAGCAGCCCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAATGCGGTAAAGCGA 567
Db 511 CAGCAGCCCGGTAAATACAGAGGTGCGAGCGTTAATCGGAATTAATGCGGCTTAAGCGC 570
QY 568 GCGTAGTGCTGTGTAAGTAGTCAAGTGTAAATCCCGGCTTAACCTGGGAACTGCATCT 627
Db 571 GCGTAGGCGGTTTGTAAAGTCAGATGTAAAGCCCGGCTCAACTGGAACTGCATTT 630
QY 628 GAACACTGTAGCTAGTAGTGTGAGGGAAGTACAAATTCAGGCTAGCGGTGAATG 687
Db 631 GAAACTGGCAGCTAGAGTGCAGTAGAGGAGGTGGAATTTCCGCTGAGCGGTGAATG 690
QY 688 CGTAGATCTGAAGGAATACCGATGGCAGAGCAGCTTCCTGGCATCATACCTGACACTG 747
Db 691 CGTAGAGATCGGAAGGAACACCACTGGCGAAGCGGCTCTGGAGTACACACTGACGCTG 750
QY 748 AGGCTCGAAGCGTGGGTAGCAAAACAGATTAGATACCTCGTGTAGTCCACCGCTAAAG 807
Db 751 AGGTGCGAAGCGTGGGAGCAAAACAGATTAGATACCTCGTGTAGTCCACCGCTAAAG 810
QY 808 ATGCTACTAGTGTGGTGGTCCCTT-GAGGACTTACTGACGAGCTAACGCAATAGTAG 866
Db 811 ATGCTACTAGTGTGGTGGTCCCTTATTTAGTATTTGTGTGAGGAGTAAACCGGATAGTAG 870
QY 867 ACCGCTGGGAGTAGCGGCCCAAGGTTAAAACTCAAAATGAATTGACGGGGCCCGACA 926
Db 871 ACCGCTGGGAGTAGCGGCCCAAGGTTAAAACTCAAAATGAATTGACGGGGCCCGACA 930
QY 927 AGCGGTGGACATGCGGTTTAAATCGATGCAAGCGGAACCTTACCTGTCTTGACAT 986
Db 931 AGCGGTGGACATGCGGTTTAAATCGATGCAAGCGGAACCTTACCGAGCCCTTGACAT 990
QY 987 ACACAGAACTCTTAGAGATACGAGTGGCTTCGGGAAATTTGTATACAGTGTGCTGATG 1046
Db 991 CTTGCGAATCTTAGAGATAGATGTTGCTTCGGGAACGAGTGACAGTGTGCTGATG 1050
QY 1047 GCTCTCTAGCTGCTGCTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTTG 1106
Db 1051 GCTCTCTAGCTGCTGCTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTTG 1110
QY 1107 TCCCTAGTTACAGCACTTCGGGTGGGAATCTTAAGGATACCTGCCAGTGACAACTGGAG 1166
Db 1111 TCCCTAGTTCCAGCACTTCGGGTGGGAATCTTAGGAGACTGCCGGTGACAAACCGGAG 1170
QY 1167 GAAGCGGGGACACGCTCAAGTTCATCTAGCCCTTAGCCAGCGGCTACACACCTGCTAC 1226
Db 1171 GAAGGTGGGACACGCTCAAGTTCATCTAGCCCTTAGCCCTTAGCGGCTGACACACCTGCTAC 1230
QY 1227 AATGGTAGGTACAGAGGGGACGCTACACAGCGATGTGATCGAATCTCAAAAGCCTATCG 1286
Db 1231 AATGGCGGTACAGAGGGGACGGAAGTCGGGAGGCCCAAGCAATCCCTTAAACCGTTCG 1290
QY 1287 TAGTCCAGATTGAGTCTGCACTCGACTCCATCAAGTAGGATCGCTAGTAATTCGGGA 1346
Db 1291 TAGTCCGGATTGAGTCTGCACTCGACTCCATCAAGTAGGATCGCTAGTAATTCGGGA 1350
QY 1347 TCAGATGCGCGGTGAATACGTTCCCGGCTTTGTACACACCGCCCTCACACATGGG 1406
Db 1351 TCAGATGCTGCGGTGAATACGTTCCCGGCTTTGTACACACCGCCCTCACACATGGG 1410
QY 1407 AGTTGATTGACCAAGAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCAGGTGTGGT 1465

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Db 1411 AGTGGATTGCACCAAGTATAGTCTTAACCTTCGGAGAGACGATTAACACGGTGTGT 1470
QY 1466 CGATGACTGGGTGAAGTCTGTAACAAGGTAGCCGTAGGGGAACCTCGGCTGATCACT 1525
Db 1471 TCATGACTGGGTGAAGTCTGTAACAAGGTAGCCGTAGGGGAACCTCGGCTGATCACT 1530
QY 1526 C 1526
Db 1531 C 1531

RESULT 5
AXX83570
ID AAX83570 standard; DNA; 1528 BP.
XX AC
XX AAX83570;
XX 21-DEC-1999 (first entry)
XX 16S rDNA gene fragment from marine bacterium, isolate TE-9.
XX Monitoring; oil; contamination; sea water; detection; flagellum;
KW Gram-negative bacterium; Proteobacteria; glucose; carbon source;
KW alkane; 16S rDNA gene; ds.
XX OS
XX Proteobacteria.
XX JF11243967-A.
XX PN
XX 14-SEP-1999.
XX PD
XX 04-MAR-1998; 98JP-0069399.
XX PF
XX 04-MAR-1998; 98JP-0069399.
XX PR
XX (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
XX PA
XX WPI; 1999-564435/48.
XX DR
XX Monitoring of oil contamination of sea water - where oil contamination
PT is evaluated by detection of a microbe having properties from e.g.
PT having no flagellum, being a Gram-negative bacterium, belonging to
PT Proteobacteria, gamma subdivision, etc.z
XX PS
XX Claim 3; Page 8; 15pp; Japanese.
XX CC
XX The invention relates to a method for monitoring oil contamination of
CC sea water by detecting, in the sea water, a microbe having the following
CC properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium;
CC (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot
CC assimilate glucose as a single carbon source; and (5) it efficiently
CC assimilates at least one of 10-30C n-alkanes. This sequence represents
CC a fragment of the 16S rDNA gene from the microbe of the invention,
CC isolate TE-9.
XX
XX Sequence 1528 BP; 361 A; 358 C; 500 G; 309 T; 0 other;
QY Query Match 75.6%; Score 1153.2; DB 20; Length 1528;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1315; Conservative 0; Mismatches 181; Indels 5; Gaps 5;
QY 30 GCGCGCAGGCTTAAACATCAAGTCGAGCGGAACGATGATAGCTTGTATTAGCGTFC 89
Db 25 GCGCGCAGGCTTAAACATCAAGTCGAGCGGAACGATGATAGCTTGTATTAGCGGTC 84
QY 90 GAGCNCOCGCGGCTGAGTAACTTAGTAATCTTACCTAGTGTAGGGGAGTACGTCTGGG 149
Db 85 GAGCGG-CGGACGGGTGAGTAAACACGCTGGGAATCTGCCATAGTGGGGGATTAATCGG 143
QY 150 GAACTCGAATTAATACCGCAT-ACGCTACGGGAGAAAGCAGGGGNTATTAGACTTG 208
Db 144 GAACTCGAATTAATACCGCATATCCCTACGCGGGGAAAGCAGGGGATCTTTCGGA 203

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QY 209 CGCTATTAGATGACCCCTAACTCGGATTAAGTATAGTGGTGGGTAAGAGGCTACCTATGGCG 268
Db 204 CGCTGATGATGACCCCGCTCGGATTAAGTATAGTGGTGGGTAAGTGGCCACCAAGGCG 263
QY 269 AGCATCTTACTGCTGAGAGGATGATCAGCACACCGGACTGAGACACGGCCCGGA 328
Db 264 AGCATCCGTAATCTGCTGAGAGGATGGCCAGTACACCCGGGACTGAGACACGGCCCGGA 323
QY 329 CT-CTACGGGAGGACGAGTGGGGAATATTGGACAATGGNGGGAACCCCTGATCCAGCCAT 387
Db 324 CTCTACGGGAGGACGAGTGGGGAATCTTGGACATGGGCGCAGCCTGATCCAGCCAT 383
QY 388 GCGCGGTGTGAAAGAGGCTTTTGGTTGTAAGACACTTTAAGCAGTGTAAAGAGACTCT 447
Db 384 GCGCGGTGTGTAAGAGGCTTTTGGTTGTAAGACACTTTTCAAGTGTGGGAGGAGGCTTT 443
QY 448 TCGGTTAATACCCGGGACGATGACATTAAGTGTGAGATAGCAGCAATAGCAGCCGCTAATCTGTGC 507
Db 444 GGGCTAATACCTCGAGTACTTGACCTTACCTACAGAAAGACACCGGCTAATTTCTGTGC 503
QY 508 CAGCAGCCCGCTAATACAGAGGGTGCAGCGTTAATCGGAATTTACTGGGCGTAAAGCGA 567
Db 504 CAGCAGCCCGCTAATACAGAGGGTGCAGCGTTAATCGGAATTTACTGGGCGTAAAGCGC 563
QY 568 GCGTAGTGTGCTGATTAAGTCAATGTGAATCCCGGGCTTTAACCCTGGGAATCTCATCT 627
Db 564 GCGTAGGCGGTGTGTTAAGTCCGATGTGAAGCCCGAGGCTCAACCTTGAATTTGCTCC 623
QY 628 GAACTGTATTAGCTAGATAGTGTGAGAGGAGTGAAGATTTCAAGTGTAGCGGTGAATG 687
Db 624 GATACTGGCACGCTAGAGTGCAGTACAGAGGAGTGTGAATTTCCGGTGTAGCGGTGAATG 683
QY 688 CGTAGAGATCTGAAGGAATACCGATGGCGAGAGCGAGCTTCTGTGSCATCATCTGACATG 747
Db 684 CGTAGAGATCGGAAGGAACACACAGTGGCGAGGCGGCTCTCTGAGCTGACACTGACGCTG 743
QY 748 AGGCTGAAAGCGTGGGTAGCAACACAGAGTATAGTACCTGTGTAGTCCAGCGCGTAAAGC 807
Db 744 AGTGTGGAAGCGTGGGAGCAACAGGATTAAGTATCCCTGTGTAGTCCAGCGCGTAAAGC 803
QY 808 ATGTCTTACTAGTCTGTGGTCCCTTTAGGAGC-TTASTGACGCGACGTAAAGCAATAGTAG 866
Db 804 ATGTCTTACTAGTCTGTGGTCCCTTTAGTACATTTGGTGGCGCAGCTAACGCGATAAGTAG 863
QY 867 ACCGCTTGGGAGTACGGCGCGAGGTTAAACTCAATGAATTCAGCGGGGCGCGACA 926
Db 864 ACCGCTTGGGAGTACGGCGCGAAGTTAAACTCAATGAATTCAGCGGGGCGCGACA 923
QY 927 AGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGGAAGACCTTACCTGCTTGTGACAT 986
Db 924 AGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGGAAGACCTTACCGGCTTGTGACAT 983
QY 987 ACACAGAATCTTTAGAGATACGAGAGTGCCTTCGCGGAATTTGTGATACAGGTGCTGCATG 1046
Db 984 CTTGCGAACTTTCTAGAGATAGATTGGTGCCTTCGCGGAGCGCAGTGTGCTGCATG 1043
QY 1047 GCTGTGCTGACCTGCTGCTGAGATGTTGGGTTAAGTCCCGCAGCAGCGCAACCCCTTG 1106
Db 1044 GCTGTGCTGACCTGCTGCTGAGATGTTGGGTTAAGTCCCGTAAAGCGCAGCGCAACCCCTTG 1103
QY 1107 TCTTAGTTTACCAGCACTTCGGGTGGGAATCTTAAGGATACCTGCAGTGACAAATGCGAG 1166
Db 1104 TCTTAGTTTACCAGCACTTCGGGTGGGAATCTTAAGGATACCTGCAGTGACAAATGCGAG 1163
QY 1167 GAAGCGGGGAGCAGCTCAAGTATCATGCGCCCTTTACGACCGAGGCTTACACAGCTGCTAC 1226
Db 1164 GAAGTGGGAGCAGCTCAAGTATCATGCGCCCTTTACGCGCTGGGCTTACACAGCTGCTAC 1223
QY 1227 AATGTTAGTACAGAGGCGAGCTACACAGCATGTGATGCGAATCTCAAAAGACCTATCG 1286
Db 1224 AATGTTAGTACAGAGGCTTTCGGAAGTCGCGAGGCGGAGCTTAATCTCTCAAAAGCAATCG 1283

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Db 991 CCTTGGAACTTTCTAGAGATGATTGGTGGCTTGGGAGCAAGTACAGGTGCTGCATG 1050
 QY 1047 GCTGCTCAGTCTGTCGTGAGATGTTGGTTAAGTCCGCAACAGACGCCACCCCTTG 1106
 Db 1051 GCTGCTCAGTCTGTCGTGAGATGTTGGTTAAGTCCGCAACAGACGCCACCCCTTG 1110
 QY 1107 TCCTTACTTACCAAGCACTTCGGTGGGAGTCTTAAGGATACGTCAGTACCAAACTGGAG 1166
 Db 1111 TCCTTACTTACCAAGCACTTCGGTGGGAGTCTTAAGGATACGTCAGTACCAAACTGGAG 1170
 QY 1167 GAAGCGGGGACGACGTCATGTCATGTCGCTTACGACCAAGGCTACACAGCTGCTAC 1226
 Db 1171 GAAGGTGGGACGACGTCATGTCATGTCGCTTACGACCAAGGCTACACAGCTGCTAC 1230
 QY 1227 AATGGTATGACAGAGGAGCTACACAGCGATGTCAGTACGAAATCTCAAAAGCTATCG 1286
 Db 1231 AATGGCGGTACAGAGGAGGAGTCCGAGGCGGAGCAAAATCCCTTAAACCGCTTCG 1290
 QY 1287 TAGTCCAGATTGAGTCTGCACTCGACTCCATGCAATGAGTATGCTAGTAAATCGCGGA 1346
 Db 1291 TAGTCCGGAATGAGTCTGCACTCGACTCCATGCAATGAGTATGCTAGTAAATCGGAA 1350
 QY 1347 TCAGAATGCGCGGTGAATACGTTCCCGGCTTGTACACACGCGCGCTCAACACATGGG 1406
 Db 1351 TCAGAATGCGCGGTGAATACGTTCCCGGCTTGTACACACGCGCGCTCAACACATGGG 1410
 QY 1407 AGTTGATGACACAGAGTGGTTAGCTTAA-CCTTATGAGGCGGATCAACACGCTGTGGT 1465
 Db 1411 AGTGGATTGCACAGAGTGGTTAGTCTTAACCTTCGGGAGGACGATCAACACGCTGTGGT 1470
 QY 1466 CGATGACTGGGTGAAGTCTGTAACAGTAGCCGTAGGAGACCTTCGGCTGGATCACT 1525
 Db 1471 TCATGACTGGGTGAAGTCTGTAACAGTAGCCGTAGGAGACCTTCGGCTGGATCACT 1530
 QY 1526 C 1526
 Db 1531 C 1531
 RESULT 8
 AAX83564
 ID AAX83564 standard; DNA; 1529 BP.
 XX AAX83564;
 AC AAX83564;
 XX 21-DEC-1999 (first entry)
 XX 16S rDNA gene fragment from marine bacterium, isolate ST-T1.
 DE DE
 DE DE
 KW Monitoring; oil: contamination; sea water; detection; flagellum;
 KW Gram-negative bacterium; Proteobacteria; glucose; carbon source;
 KW alkane; 16S rDNA gene; ds.
 XX Proteobacteria.
 OS JP11243967-A.
 XX JP11243967-A.
 XX 14-SEP-1999.
 XX 04-MAR-1998; 98JP-0069399.
 XX 04-MAR-1998; 98JP-0069399.
 XX (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
 XX WPI; 1999-564435/48.
 XX Monitoring of oil contamination of sea water - where oil contamination
 PT is evaluated by detection of a microbe having properties from e.g.
 PT having no flagellum, being a Gram-negative bacterium, belonging to
 PT Proteobacteria, gamma subdivision, etc.2
 XX ClaIm 3; Page 5; 15pp; Japanese.

XX The invention relates to a method for monitoring oil contamination of
 CC sea water by detecting, in the sea water, a microbe having the following
 CC properties: (1) it has no flagellum; (2) it is a Gram-negative bacterium;
 CC (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot
 CC assimilate glucose as a single carbon source; and (5) it efficiently
 CC assimilates at least one of 10-30C n-alkanes. This sequence represents
 CC a fragment of the 16S rDNA gene from the microbe of the invention,
 CC isolate ST-T1.
 XX
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 Best Local Similarity 86.7%; Pred. No. 0;
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 QY 209 CCGTATTAGTAGAGCTTAAGTCGGATTAGCTAGTGGGTAAAGGCTTACCATTGGCG 268
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 QY 329 CT-CTACGGGAGGACGAGTGGGGATATTGGCAATGNGGGAACCTTGATCCAGCCAT 387
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 QY 508 CAGCAGCGCGGTAATACAGAGGTCGCAAGCTTAATCGGAATTACTGGCGCTAAAGCGA 567
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 QY 628 GAACTGTTAGGCTAGTAGTAGTACAGAGGAGTAGAATTCAGGTGTAGCGGTGAATG 687
 Db 624 GAACTGTCAGGCTAGTAGTAGTACAGAGGAGTAGAATTCAGGTGTAGCGGTGAATG 683
 QY 688 CGTAGAGATCTGAAGGAATACCGGAGGAGGAGGCTTCTTGGCATCATACTGACACTG 747
 Db 684 CGTAGAGATCTGAAGGAATACCGGAGGAGGAGGCTTCTTGGCATCATACTGACACTG 743
 QY 748 AGGCTCGAAAGCGTGGGTAGCAAAACAGGATTAGATACCTTGGTAGTCCACGCGCTAACG 807
 Db 744 AGGTCGAAAGCGTGGGTAGCAAAACAGGATTAGATACCTTGGTAGTCCACGCGCTAACG 803
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Db 664 CGTAGATATAGGAAGAAATACCGATGCGGAAGGAGTCTCTGCGCATCACTGACACATG 723
QY 748 AGCTGTGAAGGCTGGGTAGCAAAACAGATTAATGATACCTGTGTAGTGTAGGAGGAG 807
Db 724 AGTGTGAAGGCTGGGTAGCAAAACAGATTAATGATACCTGTGTAGTGTAGGAGGAG 783
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Db 904 CGCGTGTAGCTGTGGTAAATGATGCAACGCGGAGAACCTTACCTGTGTGTGACATC 963
QY 988 CACAGAACTCTGTAGAGATACAGAGTGCCTTCGGGAATGTGTATACAGTGTGTGTATG 1047
Db 964 CATGTAACTTCCAGAGATGATGGTGCCTTCGGGAATGTGTATACAGTGTGTGTATG 1023
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Db 1384 AGT 1443
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RESULT 14
AAH77497
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XX
AC AAH77497;

XX 20-NOV-2001 (first entry)
XX Pseudomonas jessenii P161 coding sequence fragment.
XX Polyhydroxyalkanoate; PHA; ds.
XX Pseudomonas jessenii.
XX JP2001178485-A.
XX 03-JUL-2001.
XX 27-DEC-1999; 99JP-0371865.
XX 27-DEC-1999; 99JP-0371865.
XX (CANO) CANON KK.
XX WPI; 2001-586288/66.
XX Production of a polyhydroxyalkanoate useful as a functional polymer -
XX Disclosure; Page 9; 12pp; Japanese.
XX The present invention describes a method of producing a
XX polyhydroxyalkanoate (PHA) using a microbe. This may be Pseudomonas
XX cichorii YN2, Pseudomonas cichorii H45 or Pseudomonas jessenii P161. The
XX PHA produced using the method of the invention is useful as a functional
XX polymer. The present sequence is a fragment of the P. jessenii coding
XX sequence.
XX Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;
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Best Local Similarity 85.9%; Pred. No. 0;
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QY 269 ACATCTGTAGT 328
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QY 388 GCGCGGT 447
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QY 448 TCGGTTTAATACCGGAGGAGT 507
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Db	424	TAACCTAATPACCTTAGTGTGTTTTCACCTTACCGACAGAAATAGCACCGGCTAACTCTGTGC	483
QY	508	CAGCAGCCCGGTAAATACAGAGGGTGCAGCGTTAAATCGGAATTACTGGGCGTAAAGCGA	567
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QY	1407	AGTTGATGACCAAGATGTTTAGCCCTAA - CTTAGTGGGGCCGATCACACAGGTGTGGT	1465

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 01:43:45 ; Search time 3470.79 seconds
(without alignments)
10685.946 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: em_estin:*

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6: em_estpl:*

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9: gb_esti:*

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11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_pro:*

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25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gssi:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	617	40.4	1084	29	B2439740
3	616.8	40.4	1054	28	BH647750
4	606.8	39.8	1044	29	B2463550

C 5	606.8	39.8	1051	29	B2494182
C 6	606.6	39.8	1053	29	B2447500
C 7	603.6	39.6	1010	29	B2431523
C 8	602.6	39.5	1031	28	BH656222
C 9	600.4	39.3	1077	29	B2450751
C 10	595.2	39.0	1016	29	B2426201
C 11	591.8	38.8	1079	28	BH705272
C 12	582.4	38.2	741	14	CD042372
C 13	571.6	37.5	1143	28	BH814966
C 14	571.6	37.4	974	29	B2440868
C 15	562	36.8	951	28	BH651765
C 16	557.4	36.5	1096	29	B2502068
C 17	556.4	36.5	901	29	B2461852
C 18	552.6	36.2	977	29	B2459292
C 19	552.4	36.2	1068	29	B2576668
C 20	549	36.0	899	29	B2685785
C 21	548.6	36.0	918	29	B2437960
C 22	548.4	35.9	699	14	CD043647
C 23	547.2	35.9	1010	29	B2568539
C 24	545	35.7	1205	29	B2566538
C 25	542	35.5	947	29	B2464837
C 26	540.6	35.4	1069	29	B2474941
C 27	537.8	35.2	674	14	CD044496
C 28	535.6	35.1	1030	29	B2463792
C 29	533	34.9	641	14	CD040169
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C 31	531.2	34.8	1106	29	B2469058
C 32	527.8	34.6	981	29	B2442959
C 33	524.4	34.4	873	28	BH705306
C 34	522.4	34.2	882	29	B2455326
C 35	519.2	34.0	837	29	B2483676
C 36	518.6	34.0	846	28	BH562180
C 37	518.2	34.0	842	28	BH482629
C 38	517.8	33.9	862	28	BH527452
C 39	516.6	33.9	953	29	B2440283
C 40	515.2	33.8	831	29	B2501502
C 41	514.4	33.7	835	28	BH552149
C 42	514.2	33.7	889	29	B2428275
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DEFINITION LLMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
ACCESSION BH771024
VERSION BH771024.1
KEYWORDS GSS.
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
REFERENCE 1 (bases 1 to 6499)
AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments, (2002) in press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain ILL403 is ywga (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.

BH771024 6499 bp DNA linear GSS 01-MAY-2002
LLMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.

BH771024
BH771024.1
GI:20373981

Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

1 (bases 1 to 6499)

Bolotin,A., Ehrlich,S.D. and Sorokin,A.

Studies of genomes of dairy bacteria Lactococcus lactis

Sci. Aliments, (2002) in press

Contact: Sorokin A

Genetique Microbienne

INRA

CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France

Tel: 33 1 34 65 25 16

Fax: 33 1 34 65 25 21

Email: sorokine@jouy.inra.fr

best homologue in strain ILL403 is ywga (78%)

Class: shotgun

High quality sequence start: 30

High quality sequence stop: 6471.


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total DNA inserted into pHOS1 using BstXI linkers"
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ORIGIN
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Best Local Similarity 77.13; Pred. No. 6e-157;
Matches 795; Conservative 0; Mismatches 210; Indels 26; Gaps 4;
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DB 1010 GATTAGCTAGTGTGGTAAAGGCTTACCATGGCGAGCATCTGTAGCTGTCTGAGAG 951
QY 292 GATGATCAGCACACCGGAGCTGAGACACGCGCCGGACT-CTACGGGAGGCGACAGTGGG 350
DB 950 GATGATCAGCACACCTGGGACTGAGACACGCGCCGGACTCTACGGGAGGCGACAGTGGG 891
QY 351 GAATATGGCAATGNGGSAACCTGTATCCAGCCATGCGCGTGTGTGAAGAGGCTT 410
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DB 673 CGGTCAATCCAGGCTCAACCTGGACAGCGGTGGAACCTACCAAGCTTGATGACG 614
QY 651 GAGAGGAGTAGAATTCAGTGTAGCGGTAAATCCGTAGAGATCTGAAGAGATACCG 710
DB 613 TAGGGCAGAGGGAATTCGGTGGAGCGGTGAATCGTAGAGATCGGAAAGAACACCA 554
QY 711 ATGGGAGGAGCGCTCTCGCATCATCTACACTGAGCTCGAAGCGTGGGTAGCAA 770
DB 553 ACGGGAAGACACTCTGCTGGGCGCACACTGACACTGAGAGACGAAGTAGGGAGCGA 494
QY 771 ACAGGATTAGATACCTCTGTAGTCCACCGCTTAACCATGTCTACTAGTTCGTTGGTCC 830
DB 493 ATGGGATTAGATACCCCACTAGTCTAGCCGTAAACGATGATAGTACGCTGTGGCTA 434
QY 831 TTGAGGACT-TAGTACGAGCTACGCAATAAGTAGACCGCTGGGAGTAGCGCCGCA 889
DB 433 TCGACCGCTGCACTGTCTGAGTAAAGCGTTAAAGTATCCCGCTGGGAGTAGCTTCGCA 374
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DB 373 AGAATGAACCTCAAAAGGATTCAGCGGGGCGCCACAGCGGTGGAGCATGTGGTTAAT 314
QY 950 TCGATGCAACCGGAAGACCTTACCTGTGTTGATACACAGAAATCTTTGAGACATACG 1009
DB 313 TCGATGCAAAAGGAGAACCTTACCGAGGCTTGACATCGCGCAATCTCTTGAAGAGA 254
QY 1010 AGAGTGCCTTCGGGAATTTGTGATACAGTGTGATGGCTGTGCTGAGCTGTGTCGTA 1069
DB 253 GGGTGTGCTTCGGGAACCGGACACAGGTGTGATGGCTGTGCTGAGCTGTGTCGCTAA 194
QY 1070 GATGTGGGTTAGTCCCGACAGGCGCAACCCCTTTCCTTAGTTACAGCACTTCGGG 1129
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DB 134 TTGGAAACCTGACAGACTCCCGGTGATTAAGCCGGAGGAGGTGAGGATGACGTCAAGTC 75
QY 1190 ATCATGGCCCTTAGCAGCAGGCTACACACGTCGTACATGGTGTAGGTACAGAGGCACT 1249
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QY 1250 ACACAGCGCATG 1260
DB 14 ATCCCGCGAGG 4
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BH656222/c
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DEFINITION BOMJ286TF BO_2_3_KB Brassica oleracea genomic clone BOMJ286,
genomic survey sequence.
ACCESSION BH656222
VERSION BH656222.1 GI:18714532
KEYWORDS GSS
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 1031)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: Tg
Class: Sheared ends.
FEATURES
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/mol_type="genomic DNA"
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/notes="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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ORIGIN
Query Match 39.58; Score 602.6; DB 28; Length 1031;
Best Local Similarity 75.74; Pred. No. 1.2e-156;
Matches 795; Conservative 0; Mismatches 230; Indels 25; Gaps 3;
QY 331 CTACGGGAGGAGCAGTGGGGAATATGGACAATGGNGGAACCTGTATCCAGCATGCC 390
DB 1027 CTACGGGAGGAGCAGTGGGGAATATTCGCAATGGGGAAGCCGTGACGGCAATGCC 968
QY 391 GCGTGTGTGAAGAGGCGCTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAGACTCTTCG 450
DB 967 GCGTGGAGTAGAGGCTTACGGGCTCTCACTCTTTTCCAGAGAAAG-----916
QY 451 GTTAATATCCCGGAGCATGATAGTCAGTAATAGCACCAGGCTAACTCTGTGCGAG 510
DB 915 -----CAATGACGGTATCTGGGGAATAGCATCGCTAACTCTGTGCGAG 871
QY 511 CAGCCGCGGTAAATACAGAGGTCACAGGTTAATCGGAATTAATCTGGCGGTAAAGCGAG 570
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 Db 750 ACTACCAAGCTGTAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 691
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 QY 751 CTCGAAGCGTGGGTAGCAACAGAGATAGTACCTGCTGCTAGTCTCCACCGCTTAACGATG 810
 Db 630 GACCAAGCTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 571
 QY 811 TCTACTAGTGTGGTCCCTTGGAGGACT-TAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 869
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 QY 870 GCCTGGGAGTACGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 929
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 QY 1170 GCGGGGAGCAGCTCAAGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1229
 Db 211 GGTGAGGATGACGCTCAAGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 152
 QY 1230 GGTAGTGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1289
 Db 151 GCGCGGACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 92
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 VERSION BZ450751.1 GI:26721334
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 1077)

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other_GSSs: BOMB063TF
 Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR

Class: sheared ends.

Location/Qualifiers

FEATURES

source

1..1077
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone_lib="BO_1.6.2_KB_tot"
 /note="Vector: pBOS1; Site 1: BstXI; 1.6-2 kb sheared
 total DNA inserted into pBOS1 using BstXI linkers"

BASE COUNT 263 a 267 c 342 g 205 t
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Query Match 39.3%; Score 600.4; DB 29; Length 1077;

Best Local Similarity 78.0%; Pred. No. 4.8e-156;

Matches 760; Conservative 0; Mismatches 211; Indels 3; Gaps 3;

QY 456 CGATGACATTAGCTGCAGAAATAGCAGCGCTAACTCTGTCCAGCAGCGCGGTAATAC 525
 Db 66 CAATGACGCTATCTGGGGAATAGCATCGCTACTCTGTCCAGCAGCGCGGTAATAC 125
 QY 526 AGAGGTGCGAGCGTTAATTCGGAATTAATCTGGGCGTAAAGCAGCGCTAGTGGCTGTAA 585
 Db 126 AGAGGATGCAAGCGTTATCCGGAATGATGGCGGTAAGCGTCTGTAGTGGCTTTTAA 185
 QY 586 GTGAGATGTGAATATCCCGGCTTAACCTGGGAACCTGCACTGAACTGTGAGCTGTAGGCTAG 645
 Db 186 GTCCGCGCTCAATCCAGGCGTCAACCTGGACAGCGGTGGAACCTACCAAGCTTGAG 245
 QY 646 TAGGTGAGAGGGAAGTGTAGAAATTCAGGTGTAGCGGTCAAAATCGGTAGAGATCTGAAGGAA 705
 Db 246 TAGGTTAGGCGCAGAGGGAATTTCCGGTGGAGCGGTGAATCCGTAGAGATCGGAAGAA 305
 QY 706 TACCGATGGCGAAGGAGCGCTTCCTGGCATCATCTGACACTGAGCGCTGAAAGCGTGGGT 765
 Db 306 CACCAAGCGGAAGCGCTCTGCTGGGCGGCACTGACACTGAGAGAGCAAGCTAGGGG 365
 QY 766 AGCAACAGGATTAGATACCTCTGGTGTAGTCCACGCGCTAAACGATCTCTACTAGTCGTTGG 825
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 QY 826 GTCCCTTTAGGACT-TAGTGACGAGCTAAACGAAATAGTAGACCGCTCGGGGAGTACGG 884
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 QY 885 CCGCAAGTTAAACTCAATGAATGANTGACGGGGGCGCCGACAGCGGTGGAGCATGTGGT 944
 Db 486 TCGCAAGATGAACCTCAAGGAATTTGACGGGGGCGCCGACAGCGGTGGAGCATGTGGT 545
 QY 945 TTAATTCGATGCAAGCGCAAGAACTTACCTGCTGTGACATACACAGATCTGTGTAGAG 1004
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BZ426201/c

LOCUS

DEFINITION BONDZ28TF BO.1.6.2_KB tot Brassica oleracea genomic clone BONDZ28,
 genomic survey sequence.

ACCESSION BZ426201

VERSION BZ426201.1 GI:26667713

SOURCE GSS.

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.

TOWN, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished

Other GSSs: BONDZ28TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

Location/Qualifiers

1..1016

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/mol_type="genomic DNA"

/strain="T01000DB3"

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/notes="Vector: PHOS1; Site.1: BstXI; 1.6-2 kb sheared
 total DNA inserted into phos1 using BstXI linkers"

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Matches 797; Conservative 0; Mismatches 209; Indels 27; Gaps 5;

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 Db 948 AGAGGATGATCAGCCACACTGGGACTGAGACACGCCCCGAGCTCTTACGGGAGGACAG 889
 QY 347 TGGGGAATATTGACAAATGNGNGGAACCTTATCCAGCATGCGCGTGTGTGAAGAAGG 406
 Db 888 TGGGGAAT-TTCGCAATGGCGGAAAGCTGACGAGCAATGCCGCTGGAGTAGAAGG 830
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 Db 829 CTTAGGGTCTCGAAGCTCTTTCCAGAGAGAG-----C 793
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 Db 792 AATGACGCTATCTGGGAATAAGCATCGCTTAACCTGTGCCAGACGCGCGGTAAATACA 733
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 Db 612 ACGGTAGGGGAGAGGAAATTTCCGCTGGAGCGGTGAAATGCGTAGAGATGTAAGGAAT 553
 QY 707 ACCGATGGCAGGCGAGCTTCTGTCATCACTACGACTGAGGCTCGAAGCGTGGGTA 766
 Db 552 ACCAAGCGGAAAGCACTCTGCTGGCGGACACTGACACTGAGAGACGAAAGCTAGGGGA 493
 QY 767 GCAACAGAGATTAGATACCTGTGTAGTCCACGCGTAAAGCATGCTTACTAGTCTTGGG 826
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 QY 827 TCCCTTGAGGACT-TAGTGAACGACTAACGCAATAGTAGACCGCTGGGAGTAGCGG 885
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 QY 1066 GTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCTTGTCTTAGTTACAGCACTT 1125
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 QY 1126 CGGTGGGAACTCTAAGGATGATGCGAGTGAACAACCTGGAGGAAGCGGGGAGCACTCA 1185
 Db 133 GAGTTTGGAACTCTAAGGATGATGCGAGTGAACAACCTGGAGGAAGCGGGGAGCACTCA 74
 QY 1186 AGTCATCATGGCCCTTACGACCGGGGTACACAGTCTGTACAATGTAGTACAGAGGG 1245
 Db 73 AGTCATCATGGCCCTTATGCTGCGGACACAGTACTACTAATGCGCGGACCAAGGGT 14
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RESULT 11

BH705272

LOCUS

BH705272

1079 bp

DNA

linear

GSS 20-FEB-2002

Db 953 ACACGTGCTATCATGG 968

RESULT 15
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genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 951)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
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genomic DNA inserted into pHS1 using BstXI linkers"
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Best Local Similarity 77.9%; Pred. No. 2.3e-145;
Matches 715; Conservative 0; Mismatches 200; Indels 3; Gaps 3;

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|||||

Qy 582 ATAGCTAGATGTAATCCCGGGCTTAACCTGGGACTGCTGTAACACTGTGTAGGCT 641
|||||
Db 66 TTAAGTCCGCGTCAATCCAGGGTCAACCTGGACGCGGTGGAACACTACCAAGCT 125
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Qy 642 AGAGTAGTGTAGAGGAAGTAGAATTTTCAGGTAGCGGTCAATCGGTAGAGATCTGAA 701
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Db 126 TGAGTACGGTATAGGGGCGAGAGGAATTTCCGGTGGAGCGGTGAAATCGGTAGAGATCGGAA 185
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Qy 702 GGAATACCGATGGCGAGGCGAGCTTCCCTGGCATATACCTGACACTGAGGCTCGAAGAGCT 761
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Db 246 GGGGAGCGAATGGGATTAGATACCCCACTAGTCTAGCCGTAAACGATGGATAGCGG 305
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Qy 822 TTGGTCCCTTGGAGCT-TAGTGACGAGCTTAACGCAATAAGTAGACCGCGTGGGAGT 880
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Db 306 CTGTCTGATCGACCGCTGCGTGTGTAGCTTAACGGGTTAAGTATCCCGCTGGGAGT 365
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Qy 881 ACGGCGCAAGGTTTAAACTCAATGATTTGACGGGGCGGCACAAAGCGGTGGAGCATG 940
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Db 366 ACGTTCCGAGATGAACATCAAGGATTTGACGGGGCGGCACAAAGCGGTGGAGCATG 425
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|||||

Qy 1301 GTCTGCAACTCGACTCCATCAAGTAGGAATCGCTAGTAAATCGCGGATCAG-RATGCCGG 1359
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Db 785 GGTGCAACTCGCTGATGAAGCGGAATCGCTAGTAAATCGCGGATCAG-RATGCCGG 844
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Db 845 GTGAATTCGTTCCCGGGCTTGTACACACCGCCGCTACACACCATGGGAGTTGATTCACC 904
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Qy 1420 AGAAGTGGTTAGCCCTAAC 1437
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Db 905 CGAAGTCGTTACCTTAAC 922
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Job time : 3479.79 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 01:46:25 ; Search time 123.463 Seconds
(without alignments)
5455.496 Million cell updates/sec

Title: US-09-979-558A-1

Perfect score: 1526

Sequence: 1 ttgatcatgctccagatt.....acotggctggtacacctc 1526

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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2	1098.6	72.0	1501	4 US-09-793-920A-1	Sequence 1, Appl
3	1098.6	72.0	1501	4 US-09-821-016-5	Sequence 5, Appl
4	1098.6	72.0	1501	4 US-09-745-476-1	Sequence 1, Appl
5	1098.6	72.0	1501	4 US-09-748-205-1	Sequence 1, Appl
6	1076	70.5	1542	1 US-08-114-695A-1	Sequence 1, Appl
7	1069.2	70.1	1542	2 US-08-757-653-158	Sequence 158, App
8	1069.2	70.1	1542	4 US-09-465-355-2	Sequence 2, Appl
9	1069.2	70.1	1542	4 US-08-520-945-158	Sequence 158, App
10	1053.6	69.0	1518	1 US-08-114-695A-6	Sequence 6, Appl
11	1019.8	66.8	1540	4 US-09-228-184-1	Sequence 1, Appl
12	1019.8	66.8	1540	4 US-09-967-376-1	Sequence 1, Appl
13	1008.8	66.1	1830121	4 US-09-557-884-1	Sequence 1, Appl
14	1008.8	66.1	1830121	4 US-09-557-884-1	Sequence 1, Appl
15	1008.8	66.1	1830121	4 US-09-643-990A-1	Sequence 1, Appl
16	1008.8	66.1	1830121	4 US-09-643-990A-1	Sequence 1, Appl
17	1004.2	65.8	1484	2 US-08-632-470-53	Sequence 53, Appl
18	983.2	64.4	1449	4 US-09-602-417-1	Sequence 1, Appl
19	932.8	61.1	1474	1 US-08-114-695A-8	Sequence 8, Appl
20	931.8	61.1	1536	2 US-08-642-229A-1	Sequence 1, Appl
21	927.8	60.5	1536	1 US-08-114-695A-7	Sequence 7, Appl
22	922.6	60.5	1451	3 US-09-342-579-1	Sequence 1, Appl
23	922.6	60.5	1451	4 US-09-617-854A-1	Sequence 1, Appl
24	897.2	58.8	1473	1 US-08-114-695A-2	Sequence 2, Appl
25	896.4	58.7	1452	2 US-08-643-229A-2	Sequence 2, Appl
26	891	58.4	1495	4 US-09-063-898-1	Sequence 1, Appl
27	865.4	56.7	1455	2 US-08-642-229A-3	Sequence 3, Appl

28 842.4 55.2 1512 3 US-08-995-960-2 Sequence 2, Appl

29 830.6 54.4 1506 3 US-09-198-955A-13 Sequence 13, Appl

30 830.6 54.4 1506 4 US-09-694-531-13 Sequence 13, Appl

31 830 54.4 1438 4 US-09-347-001-1 Sequence 1, Appl

32 824.6 54.0 1494 2 US-08-632-470-49 Sequence 49, Appl

33 821.2 53.8 1516 3 US-09-248-528-3 Sequence 3, Appl

34 821.2 53.8 1516 3 US-09-549-108-3 Sequence 3, Appl

35 821.2 53.8 1516 3 US-09-549-111-3 Sequence 3, Appl

36 821.2 53.8 1516 3 US-09-549-106-3 Sequence 3, Appl

37 821.2 53.8 1516 3 US-09-550-394-3 Sequence 1, Appl

38 821.2 53.8 1516 4 US-09-426-868-1 Sequence 1, Appl

39 820.4 53.8 1436 4 US-09-347-001-2 Sequence 2, Appl

40 818.6 53.6 1555 2 US-08-757-653-160 Sequence 160, App

41 818.6 53.6 1555 4 US-08-520-946-160 Sequence 160, App

42 818 53.6 1452 1 US-08-276-943-1 Sequence 1, Appl

43 818 53.6 1452 2 US-08-716-841-1 Sequence 1, Appl

44 816.6 53.5 1551 4 US-09-375-932A-8 Sequence 8, Appl

45 814.6 53.4 1450 4 US-09-339-159B-33 Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-08-299-810A-27

; Sequence 27, Application US/08299810A

; Patent No. 5721097

; GENERAL INFORMATION:

; APPLICANT: Rossau, Rudi

; APPLICANT: Van Heuverswyn, Hugo

; TITLE OF INVENTION: HYBRIDIZATION PROBES FOR THE

; TITLE OF INVENTION: DETECTION OF BRANHAMELLA CATARRHALIS STRAINS

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant & Gould

; STREET: 3100 No. 5721097west Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/299,810A

; FILING DATE: 01-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Hillson, Randall A.

; REGISTRATION NUMBER: 31,838

; REFERENCE/DOCKET NUMBER: 8076.70-US-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-332-5300

; TELEFAX: 612-332-9081

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1485 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Branhamella catarrhalis

; IMMEDIATE SOURCE:

; CLONE: 16S rRNA Gene

US-08-299-810A-27

Query Match 78.3%; Score 1195; DB 1; Length 1485;

Best Local Similarity 90.6%; Pred. No. 0;

Matches 1352; Conservative 0; Mismatches 128; Indels 12; Gaps 7;

Db	1072	TACACGGACTCGGTCGGGAACCTTAAGGATATCTCCAGTGACAACTGGAGGAAGCGG	1131
Qy	1175	GGACAGCTCAAGTCAATCATGAGCCCTTACGACACAGGCTACACACGTCGTACAAATGGTAG	1234
Db	1132	GGACAGCTCAAGTCAATCATGAGCCCTTACGACACAGGCTACACACGTCGTAACAATGGTTG	1191
Qy	1235	GTACAGAGGGCAGCTACACACGAGTGGATGGAATCTCAAAAAGCCTATPCTGATCCAG	1294
Db	1192	GTCAAAAGGGTTGCTACACACGAGTGTGATGTAATCTCAAAAAGCAATCTGATCCGG	1251
Qy	1295	ATTGGAGTCTGCAACTCGACATCCAGTAAAGTAGGAATCGCTAGTAATCGCGGATCAGAATG	1354
Db	1252	ATTGGAGTCTGCAACTCGACATCCAGTAAAGTAGGAATCGCTAGTAATCGCAGATCAGAATG	1311
Qy	1355	CCGCGGFGAATACGTTCCCGGGCCCTTGACACACCGCCCGCTCACACATGGAGGATGATT	1414
Db	1312	CTGCGGTGAATACGTTCCCGGGCCCTTGACACACCGCCCGCTCACACATGGAGTGTATC	1371
Qy	1415	GCACACAGAGTGGTAGCCTTAACCTTAGTAGGGGCGATCACCACGCTGCTGTCGATCACTG	1474
Db	1372	TCACAGAGTGGTAGCCTTAACCCA-AGAGGGCGATCACCACGCTGGGTGATGACTG	1430
Qy	1475	GGGTGAAGTCGTAACAAGGTAGCCGTAGGCGAACCTGGCGCTGGATCACCTC	1526
Db	1431	GGGTGAAGTCGTAACAAGGTAGCCGTAGGCGAA-CTGCGGCTGGATCACCTC	1481

RESULT 2
 US-09-793-920A-1
 ; Sequence 1, Application US/09793920A
 ; Patent No. 6479621
 ; GENERAL INFORMATION:
 ; APPLICANT: Canon Inc.
 ; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanol
 ; FILE REFERENCE: 4396021
 ; CURRENT APPLICATION NUMBER: US/09/793,920A
 ; CURRENT FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 1
 ; SEQ ID NO 1
 ; LENGTH: 1501
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas jessenii 161 strain.
 US-09-793-920A-1

Qy	30	GGCGCAGGCTTAAACACATGCAATCGAGCGGAACGATGATAGCTTGCTATTAGCGCTC	89
Db	9	GGCGCAGGCTTAAACACATGCAATCGAGCGG--ATGACGGGAGCTTGCTCTGAATTCA	66
Qy	90	GAGCGCCGGAAGGGTGTAGTAATCTACTAGGAATCTACCTAGTGTGGGGATAGCTCGGG	149
Db	67	G---CGCGGAGCGGTGTAGTAATGCTTAGGATCTCCCTGTTAGTGGGGACACGCTCTC	123
Qy	150	GAAACTCGAATTAATACCCGATACCT-CTACGGGGAAGACAGGGGNTCAATTAGACCTTG	208
Db	124	GAAAGGACGCTAATACCGCATACGTCTCTACGGGGAAGACAGGGGACCTTCGGGCTTG	183
Qy	209	GCCTATTAGATGACCTTAGTCGGAATTAGCTAGAGTGGGTAAAGCCCTACCATGGCG	268
Db	184	GCCTATCAGATGAGCCCTAGTTCGGATAGTGTAGTGGTAGGATGATGGCTCACCAGGCG	243
Qy	269	ACGATCTGTAGCTGGTCTGTAGAGGATGATCAGCCACACCGGSACTGAGACACGGCCCGGA	328
Db	244	ACGATCCGTAACTGGTCTGTAGAGGATGATCAGTCACTTGGACTGAGACACGCTCCAGA	303
Qy	329	CT-CTACGGGAGCAGCTGGGGAATTTGGACAATGNGGGAACCTGATCCAGCCAT	387
Db	304	CTCTACGGGAGCAGCTGGGGAATTTGGACAATGNGGGAAGCTGATCCAGCCAT	363

QY 388 GCGCGTGTGTGAAGAGCGCTTTTGGTTGTAAGACCTTTAAGCAGTGAAGAGACTCT 447
Db 364 GCGCGTGTGTGAAGAGCGCTTTTGGTTGTAAGACCTTTAAGCAGTGAAGAGACTCT 423
QY 448 TCGGTTAATACCGGGACGATGATGATGATGATGATGATGATGATGATGATGATG 507
Db 424 TAACCTAATAGTTAGTTGTTGACCTTACCGAGATTAAGCCGGCTTAAGTCTGTC 483
QY 508 CAGCAGCGCGGTAAATACAGAGGCTCAAGCGTTAATCGGAATTACTGGCGCTAAAGCG 567
Db 484 CAGCAGCGCGGTAAATACAGAGGCTCAAGCGTTAATCGGAATTACTGGCGCTAAAGCG 543
QY 568 GCGTAGTGGCTTGAATAGTCAATGTAATCCCGGGCTTAAGCAGTGAAGAGACTCT 627
Db 544 GCGTAGTGGCTTGAATAGTCAATGTAATCCCGGGCTTAAGCAGTGAAGAGACTCT 603
QY 628 GAACTGTGTAGCTAGTGTAGTGTAGGAGGAGTGAATTTACGTTGATGCTGAATG 687
Db 604 ARACTGACAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 663
QY 688 CGTAGAGTCTGAGAGGAGTGAATTTACGTTGATGCTGAATG 747
Db 664 CGTAGATATAGAGGAGGAGTGAATTTACGTTGATGCTGAATG 723
QY 748 AGCTCGAAGCGTGGGTAGTGAATTTACGTTGATGCTGAATG 807
Db 724 AGTGGGAAGCGTGGGTAGTGAATTTACGTTGATGCTGAATG 783
QY 808 ATCTCTACCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 867
Db 784 ATCTCTACCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 843
QY 868 CCGCTGGGAGTACCGCGGAGGTTAACTCAAACTCAAACTCAAACTCAAACTCAAA 927
Db 844 CCGCTGGGAGTACCGCGGAGGTTAACTCAAACTCAAACTCAAACTCAAACTCAAA 903
QY 928 GCGGTGAGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 987
Db 904 GCGGTGAGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 963
QY 988 CACAGAACTCTGAGAGTACGAGTGGCTTGGGGAATGTTGATACAGTGTGTGATGG 1047
Db 964 CAATGAACTCTGAGAGTACGAGTGGCTTGGGGAATGTTGATACAGTGTGTGATGG 1023
QY 1048 CTCTCTGAGCTGCTGCTGAGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1107
Db 1024 CTCTCTGAGCTGCTGCTGAGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1083
QY 1108 CTTAGTTACAGCAC-CTCGGTTGGGAACTCTAAGGATGATGCTGACGATGACAACTGGAG 1166
Db 1084 CTTAGTTACAGCAC-CTCGGTTGGGAACTCTAAGGATGATGCTGACGATGACAACTGGAG 1143
QY 1167 GAAGCGGGAGCAGCTCAAGTCAATGAGCTTCAAGGAGTGAAGTGAAGTGAAGTGAAG 1226
Db 1144 GAAGTGGGGAGTCAAGTCAATGAGCTTCAAGGAGTGAAGTGAAGTGAAGTGAAG 1203
QY 1227 AATGTTAGTACAGAGGAGCAGTCAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1286
Db 1204 AATGTTAGTACAGAGGAGCAGTCAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1263
QY 1287 TAGTCCAGATGAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1346
Db 1264 TAGTCCAGATGAGTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1323
QY 1347 TCAGATGCGCGGTGAATAGCTTCCCGGGCTTGTACACAGCGCGCTGACACAGTGG 1406
Db 1324 TCAGATGCGCGGTGAATAGCTTCCCGGGCTTGTACACAGCGCGCTGACACAGTGG 1383
QY 1407 AGTTGATGCACAGAGTGTGTAGCTTAA-CTTAGTGGGCGGATCACCACCGTGTGT 1465
Db 1384 AGTGGTTCACAGAGTGTGTAGCTTAA-CTTAGTGGGCGGATCACCACCGTGTGT 1443

QY 1466 CGATGACTGGGTGAAGTCTGATACAGAGTACCGCTAGGGGAACCTCGGCTGGATCAC 1523
Db 1444 TCATGACTGGGTGAAGTCTGATACAGAGTACCGCTAGGGGAACCTCGGCTGGATCAC 1501
RESULT 3
US-09-821-016-5
; Sequence 5, Application US/09821016
; Patent No. 648591
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enz.
; FILE REFERENCE: 4051021
; CURRENT APPLICATION NUMBER: US/09/821,016
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
; FEATURE:
US-09-821-016-5
Query Match
Best Local Similarity 72.08; Score 1098.6; DB 4; Length 1501;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;
QY 30 GCGGCGAGCTTAACACATGCTAGCTGAGCGAAGACGATGATGCTGCTGATGAGCTC 89
Db 9 GCGGCGAGCTTAACACATGCTAGCTGAGCGG--ATGACGGGAGCTGCTGCTGATTC 66
QY 90 GAGCNGCGGAGCGGTGAGTAACTAGGATCTTACCTAGTCTGAGTGGGAGTACTCGGG 149
Db 67 G---CGGCGAGCGGTGAGTAACTAGGATCTGCTGCTGAGTGGGAGTACTCGGG 123
QY 150 GAACTCGGAATTAATACCGATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
Db 124 GAGAGGAGCTTAATACCGATACGTCTTACCGGAGAAAGCAGGGGACCTTCGGGCTTG 183
QY 209 CGCTATTAGTACGCTTAATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 268
Db 184 CGCTATTAGTACGCTTAATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 243
QY 269 ACATCTGTAGTGTGCTGAGAGGATGATCAGCCACCGGAGTGTGAGTGTGAGTGTGAGTGTG 328
Db 244 ACATCTGTAGTGTGCTGAGAGGATGATCAGCCACCGGAGTGTGAGTGTGAGTGTGAGTGTG 303
QY 329 CT-CTACGGGAGCAGCAGTGGGAAATATTGGACAATGNGGAAACCTGATCCAGCCAT 387
Db 304 CTCTACGGGAGCAGCAGTGGGAAATATTGGACAATGNGGAAACCTGATCCAGCCAT 363
QY 388 GCGGCTGTGAGAGAGGCTTTTGGTTGTAAGCAGCTTTAAGCAGTGAAGAGACTCT 447
Db 364 GCGGCTGTGTAAGAGAGGCTTTTGGTTGTAAGCAGCTTTAAGTGGAGAGAGGCT 423
QY 448 TCGGTTAATACCGGGAGCAGTGAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 507
Db 424 TAACCTAATAGTTAGTTGTTGACCTTACCGAGATTAAGCCGGCTTAAGTCTGTC 483
QY 508 CAGCAGCGCGGTAAATACAGAGGCTCAAGCGTTAATCGGAATTACTGGCGCTAAAGCG 567
Db 484 CAGCAGCGCGGTAAATACAGAGGCTCAAGCGTTAATCGGAATTACTGGCGCTAAAGCG 543
QY 568 GCGTAGTGGCTTGAATAGTCAATGTAATCCCGGGCTTAAGCAGTGAAGAGACTCT 627
Db 544 GCGTAGTGGCTTGAATAGTCAATGTAATCCCGGGCTTAAGCAGTGAAGAGACTCT 603
QY 628 GAACTGTGTAGCTAGTGTAGTGTAGGAGGAGTGAATTTACGTTGATGCTGAATG 687
Db 604 ARACTGACAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 663
QY 688 CGTAGAGTCTGAGAGGAGTGAATTTACGTTGATGCTGAATG 747

Db 664 CTAATATAGGAAGGACACAGTGGCGAGGCGACCACTGGAGTATAGTACACTG 723
Qy 748 AGGCTCGAAAGCGTGGGTAGCAACAGAGATAGATACCTGGTAGTCCAGCGCTAAACG 807
Db 724 AGGTCCGAAAGCGTGGGAGCAACAGAGATAGATACCTGGTAGTCCAGCGCTAAACG 783
Qy 808 ATGTCTACTAGTCTGGTGGTCCCTTCAGGACTTAGTACGACCTAACCCATATAGTAGA 867
Db 784 ATGTCAACTAGCCTGGGAGCCTTGAGCTCTTAGTGGCGAGCTAACCCATATAGTTGA 843
Qy 868 CGCCTTGGGGAGTAGCGGCCCAAGGTAAAACTCAAAATGAATTAAGTAAAGTAAAGTAA 927
Db 844 CGCCTTGGGGAGTAGCGGCCCAAGGTAAAACTCAAAATGAATTAAGTAAAGTAA 903
Qy 928 GCGGTGGAGCATGTGGTTAAATTCGATCGAAGCGGAAGAACCTTACTGGTCTTGACATA 987
Db 904 GCGGTGGAGCATGTGGTTAAATTCGAAAGCAAGCGGAAGAACCTTACTGGTCTTGACATC 963
Qy 988 CACAGAACTTGTAGATACGAGACTGCGCTTCGGGAATGTGATACAGTCTGCTATGG 1047
Db 964 CAATGAACTTCCAGAGATGGATGGTGGCTTCGGGAACATTTGAGACAGTCTGCTATGG 1023
Qy 1048 CTGTCTGAGTCTGTGCTGAGATGTTGGGTAAAGTCCCGCAACAGAGCGCAACCTTGT 1107
Db 1024 CTGTCTGAGTCTGTGCTGAGATGTTGGGTAAAGTCCCGTAAACAGAGCGCAACCTTGT 1083
Qy 1108 CCTTGTATACAGGAC-TTCGGTGGGAACTCTAAGATACTGCCAGTACAACTGGAG 1166
Db 1084 CTTTGTATACAGGACGATTAAGTGGGCACTCTAAGGAGACTCCCGGTGACAAACCGGAG 1143
Qy 1167 GAAGCGGGAGGACGCTCAAGTCAATCATGCGCCCTTACGACGAGGCTACACAGCTGTAC 1226
Db 1144 GAAGTGGGGATGAGCTCAATCATGCGCCCTTACGCGCTGGGCTACACAGCTGTAC 1203
Qy 1227 AATGTAGTACAGAGGCGCTACACAGGATGTGATGGAATTCATAAAGGCTATPG 1286
Db 1204 AATGTCTGATACAGAGGCTTCCAAAGCGGAGGTGGAGTAAATCCCAAAACCGATG 1263
Qy 1287 TAGTCCAGATGGAGTCTCACTGACTCCATGAGTGAATTCCTAGTAACTAGTACGCGGA 1346
Db 1264 TAGTCCGATGCGAGTCTGCACTGATGCTGGAATTCCTAGTAACTAGTAACTAGT 1323
Qy 1347 TCAGAAATCCCGGTGAATACGTTCCCGGCTTGTACACACGCGCCCTTCACACATGGG 1406
Db 1324 TCAGAAATCCCGGTGAATACGTTCCCGGCTTGTACACACGCGCCCTTCACACATGGG 1383
Qy 1407 AGTTGATTCACAGAGTGGTATGCTTAA-CTTAGTGGGGGATCACCAGCTGGTGGT 1465
Db 1384 AGTGGTTGSCACCAAGTAGTCTAGTCTAACTTCGGGAGGACGGTTACCGGTGTGAT 1443
Qy 1466 CGATGACTGGGGTGAATCTGATACAGGTAGCCGTAGGGAACTTCGGCTGGATCAC 1523
Db 1444 TCATGACTGGGTGAATCTGATACAGGTAGCCGTAGGGAACTTCGGCTGGATCAC 1501

RESULT 4

US-09-745-476-1
; Sequence 1, Application US/09745476
; Patent No. 6521429
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09/745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-09-745-476-1

Query Match 72.0%; Score 1098.6; DB 4; Length 1501;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

Qy 30 GCGCGCAGGCTTACACATGCAAGTGGAGCGGAACCATGATAGCTTGTCTANTAGGCGTC 89
Db 9 GCGCGCAGGCTTACACATGCAAGTGGAGCGG--ATGACGGGAGCTTGTCTCTGAATTC 66
Qy 90 GAGCMGCGGAGCGGCTGAGTAACTTAGGAATCTACTAGTGGGGATAGTCCGCGG 149
Db 67 G---CGCGGAGCGGCTGAGTAACTTAGGAATCTACTAGTGGGGATAGTCCGCGG 123
Qy 150 GAACTTCGAATTAATACCGATACGT-CTACGGGAGAAACAGGGGNTCAATAGACCTTG 208
Db 124 GAAAGGGAGCGCTAATACCGCATACGCTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTG 183
Qy 209 CGCTATTAGATGAGCCTTAAGTCCGATTAAGTGGGTAAAGGCTTAAAGCAAGCACTCT 268
Db 184 CGCTATCAGAGCTTAGTTCGGATTAAGTGGGTAGGTAACTGCTACACAGCGG 243
Qy 269 AGATCTGTAGTGGTCTGAGAGGATGATCACACACCGGGACTGAGACACGCGCCGGA 328
Db 244 AGATCCGCTAAGTGGTCTGAGAGGATGATCAGTCACTGGAATGAGACACGCTCCAGA 303
Qy 329 CT-CTACGGGAGCGCAGCTGGGGATATTGGCAATGGNGGGAACCCCTGATCCAGCCAT 387
Db 304 CTCCTACGGGAGCGCAGCTGGGGATATTGGCAATGGNGGGAACCCCTGATCCAGCCAT 363
Qy 388 GCGCGCTGTGGAAGAGGCGCTTTGGTGTAAAGCACTTTAAAGCAGTGAAGCAAGCTCT 447
Db 364 GCGCGCTGTGGAAGAGGCTCTCGGATTTAAAGCACTTTAAAGTGGAGGAGGCGAT 423
Qy 448 TCGGTTAATACCGGGGAGCAGTACATAGTGCAGAAATGAACACCGGCTACTCTGTGC 507
Db 424 TAACTAATAGCTTAGTGTGTTGAGCTTACCGGAGAAATGAACACCGGCTACTCTGTGC 483
Qy 508 CAGCAGCGCGGTAATACAGAGGCTGCAAGGTTAAATCGGAATTAAGTGGCGGTAAGCGA 567
Db 484 CAGCAGCGCGGTAATACAGAGGCTGCAAGGTTAAATCGGAATTAAGTGGCGGTAAGCGG 543
Qy 568 GCGTAGTGGCTGTAATAGTACAGTGTGAAATCCCGGGGCTTAACTGGGAAGTCACTCT 627
Db 544 GCGTAGTGGCTTGTAAAGTGGATGTGAAAGCCCGGGCTCAACCTGGGAAGTCACTCT 603
Qy 628 GAACTGTTAGGCTAGAGTGGAGGAGTAGAATTTCAAGTGTAGCGGTGAATG 687
Db 604 AAACTGACAGCTAGAGTGGTAGAGGGTGGTGAATTTCTGTGTAGCGGTGAATG 663
Qy 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTCGGCACTATACACTGACACTG 747
Db 664 CCGATATAGGAAGGAACACACAGTGGCGAAGGCGACCACTGAGTACTGACACTG 723
Qy 748 AGGCTCGAAGCGGGTAGCAACAGAGTATACCTGGTGGTGGTGGTGGTGGTGGTGGTGG 807
Db 724 AGGTCGGAAGCGGTGGGAGCAACAGAGTATACCTGGTGGTGGTGGTGGTGGTGGTGGTGG 783
Qy 808 ATGTCTACTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 867
Db 784 ATGTCTACTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 843
Qy 868 CGCCTGGGAGTACGSCCGCAAGGTTAAACTCAAAATGAATTAAGTGGGCGCGCGCAAA 927
Db 844 CGCCTGGGAGTACGSCCGCAAGGTTAAACTCAAAATGAATTAAGTGGGCGCGCGCGCAAA 903
Qy 928 GCGGTGGAGCATGTGGTTAAATTCGATCGAAGCGGAAGAACCTTACCTGGTGTGGACATA 987
Db 904 GCGGTGGAGCATGTGGTTAAATTCGAAAGCAAGCGGAAGAACCTTACCGGCGCTTGACATC 963
Qy 988 CACAGAACTTGTAGATACGAGAGTGGCTTCGGGAACTTGTGATACAGGCTGCTGATGG 1047
Db 964 CAATGAACTTTCAGAGATGGATGGTGGCTTCGGGAACTTGTGATACAGGCTGCTGATGG 1023

Query Match	72.0%;	Score	1098.6;	DB 4;	Length	1501;
Best Local Similarity	85.9%;	Pred. No. 0;				
Matches 1287;	Conservative	0;	Mismatches	202;	Indels	9;
Gaps	6;					
Qy	30	GGCGCAGGCTTAAACATCGAATGTCAGCGGAAACGATCATAGCTTCTGCTATTAGGCGTC	89			
Db	9	GGCGCAGGCTTAAACATCGAATGTCAGCGG--ATGACGGGAGCTTCTCTCGTAAATCA	56			
Qy	90	GAGCNGCCGACGGGTGAGTAACTACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG	149			
Db	67	G---CGGCGGACGGGTGAGTAACTGCTAGGAATCTGCTCTGCTAGTGGGGGACAACTCTC	123			
Qy	150	GAATCTCGAATTAAATCCGCACTACCT--CTACGGGAGAAACAGGGGNTCATTAGACCTTG	208			
Db	124	GAAGGGGACGCTAATACCCGATACGTCCTACGGGAGAAACAGGGGAGCTTCGGGGCTTG	183			
Qy	209	CCCATATTAGATGAGCCCTAACTCGGATAGCTAGATGGTGGGCTAAAGGCTTACCATGGCG	268			
Db	184	CGCTATCAGATGAGCCCTAGTTCGGATAGCTAGTTCGTCAGGTATGCTCCACCGGCG	243			
Qy	269	ACGATCTGTAGCTGTCTGAGAGGATGATCAGCCACACCGGACCTGAGACACCGGCCCGGA	328			

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QY 1407 AGTTGATTCCACCAGAGTGGTTAGCCCTAA-CTTAGTGGAGGCGCATCACACGGTGTGGT 1463
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Db 1384 AGTGGGTTCCACCAGAGTAGTACTAGTCTAACCTTCGGGAGCAGGTTACACCGGTGTGAT 1443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1466 CGATGACTGGGTGAAGTCGTACAAAGGTAGCCGTAGGGGAACCTCGGCTGGATCAC 1523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1444 TCATGACTGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACTCGGCTGGATCAC 1501
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-08-114-695A-1
; Sequence 1, Application US/08114695A
; Patent No 5508193
; GENERAL INFORMATION:
; APPLICANT: Mandelbaum, Raphael T.
; APPLICANT: Wackett, Lawrence P.
; TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
; TITLE OF INVENTION: WATER
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
; STREET: 3500 IDS CENTER
; CITY: MINNEAPOLIS
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,695A
; FILING DATE: 31-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEITING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600.268US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
US-08-114-695A-1

Query Match 70.5%; Score 1076; DB 1; Length 1542;
Best Local Similarity 67.2%; Pred. No. 0;
Matches 1008; Conservative 246; Mismatches 243; Indels 4; Gaps 3;

QY 30 GCGCGCAGGCTTACACATGCACTCGCGGGAACAGTAGA--TAGCTTGCTATTAGCGC 87
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Db 38 GCGCGCAGGCGCUUACACAGCAAGUCGACCGUACACGGAAGAGAGCUUGUCUUCUUGCU 97
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 88 TCGAGCNGCCGAGCGGTGAGTAATCTACTAGGAATCTACTAGTAGTGGGGGATAGCTCG 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 98 GACCAUGCGGAGCGGUGAGUAUGUUGUGGAAACUCGUCUGAGAGGGGGGANDACUAC 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 148 GCGAAATCGAATTAATACCCGATACGTCTACGGGAGAAACAGCGGGGNTCATTAGACCTT 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158 UGGAACGGUAGUACUAAACCCCAUACGUCGACAGACCAAGAGGGGACCUUGCGGCCUC 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 208 CCGCTATTAGATGACGCTTAAGTCGGATTAGCTAGATGTGGGGTAAAGGCGCTACCATGGC 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 UUGCAACGCGAUGGCGCCGAUGGGAUAGUAGUAGUGGUGUAACGCGUACCGUACCUAGGC 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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1347 TCAGAAATCCCGCGTGAATACGTTCCCGGGCTTGTACACACCGCCCGTCACACCATGGG 1406
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Db 1358 UCAGAAUCCACGGGUAUACUUCUCCGGCCUUGUACACACCGCCGUCACACCAUGGG 1417
1407 AGTTGATGTCACAGCAAGTGGTATGCCFPA--CTTAGTACGGGCGATCACCACGGTGGT 1465
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Db 1418 AGUGGGUUGCAAGAAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1477
1466 CGATCACTGGGGTGAAGTGGTACAGAGTACCGGTAGGGGAACCTCGGCTGGATCACT 1525
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Db 1478 UCAUGACUGGGUGAAGUCUACAAAGGUAACCGUAGGGGAACCCUGGUUGGACACCU 1537
1526 C 1526
1538 C 1538

RESULT 7

US-08-757-653-158
; Sequence 158, Application US/08757653
; Patent No. 5843669
; GENERAL INFORMATION:
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Lyamichev, Natasha
; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,653
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-653-158

Query Match 70.1%; Score 1069.2; DB 2; Length 1542;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 1256; Conservative 0; Mismatches 241; Indels 4; Gaps 4;
QY 30 GCGCGAGGCTTAACATCAAGTCAGCGGAAC--GATGATAGCTTGTATAGGCGT 88
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Db 38 GCGCGAGGCTTAACATCAAGTCAGCGGAAC--GATGATAGCTTGTATAGGCGT 97
QY 89 CGAGNCCGGGACGGGTGAGTAATCTAGTAATCTAGTAAGTGGGATAGTCGG 148
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Db 98 ACAGTGGCGACGGGTGAGTAATCTAGTAATCTAGTAAGTGGGATAGTCGG 157
QY 149 GGAARCTCGAATTAATCCGCAT--ACGCTACGGGAGAAACCGGGGNTCAITAGACCTT 207

158 GGAACGCTAGCTAATACCGCAFAACGTCGCAAGACCAAGAGGGGACCTTCGGGGCCTC 217
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QY 208 GGGCTATTAGTAGAGCCCTAAGTCGGATTAGCTAGTAGTGGGTAAAGGCTTACCATGGC 267
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Db 218 TTGCCATCGGATGTGCCCATAGTGGATTAGCTAGTAGTGGGTAAAGGCTTACCATGGC 277
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QY 268 GAGCATCTGTAGCTGGTCTCAGAGGATGATCAGCCACACCGGGAGTGAGACAGCGCCGG 327
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Db 278 GACGATCCCTAGCTGGTCTCAGAGGATGACCGACACCTGGAATGAGACAGGCTCCAG 337
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QY 328 ACT-CTACGGGAGGACGACGTGGGGAATATTGGACAATGSGNGGGAACCTGTATCAGCA 386
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Db 338 ACTCTACGGGAGGACGACGTGGGGAATATTGGACAATGSGNGGGAACCTGTATCAGCA 397
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QY 387 TGGCGGTGTGTAAGAAGCCCTTTGGTGTAAAGCACTTTAAGCAGTGAAGAAGACTC 446
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Db 398 TGGCGGTGTATGAAGAAGCCCTTCGGGTGTAAGTACTTTACAGGGGAGGAAGGGAG 457
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QY 447 TTCGGTAAATACCGGGGACGATGACATTAAGTGCAGAAATAGCACCGGCTACTCTGTG 506
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Db 458 TAAAGTTAATACCTTGTCTCATTGACGTTACCGCGAAGAAAGCAGCGCTACTCCGTG 517
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Db 518 CCAGCAGCGCGGTAATACAGAGGTCGAAGGTTAATCGGAATTACTGGGCGTAAAGCG 577
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QY 567 AGCTAGTGGCTGTGAATAGTCAGATGTGAATCCCGGGCTTAACTGGGAATGCTATC 626
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Db 578 CAGCGACGGCTTTGTTAAGTCAGATGTGAATCCCGGGCTCAACCTGGGAATGCTATC 637
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QY 627 TGAACCTGTAGGCTAGAGTAGGTGAGAGGAAGTAGAATTTACAGGTGACGGTGAAT 686
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Db 638 TGATACTGGCAAGCTGTAGTCTCGTAGAGGGGGTAGAATTCAGGTGTAGCGGTGAAT 697
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QY 687 GGTAGAGATCTGAAGGAATACCGATGCGGAAGGAGCTTCTCGCATCATCTACTGACAT 746
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Db 698 GGTAGAGATCTGAAGGAATACCGATGCGGAAGGAGCTTCTCGCATCATCTACTGACAT 757
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QY 747 GAGCTCGAAGCGTGGGTAGCAACAGATTAGATTACCTGTGTAGTCACGGCGTAAAC 806
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QY 807 GATGCTACTAGTCTGGTGGTCCCTTGAAGCTTGTAGTACGACGCTAACCAATTAAGTAG 866
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Db 818 GATGCTACTAGTCTGGTGGTGGTCCCTTGAAGCTTGTAGTACGACGCTAACCAATTAAGTAG 877
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QY 867 ACCGCTCGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTACGCGGGGCCCGCA 926
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Db 878 ACCGCTCGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTACGCGGGGCCCGCA 937
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 927 ACCGCTCGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTACGCGGGGCCCGCA 986
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Db 938 ACCGCTCGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTACGCGGGGCCCGCA 997
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 987 ACACAGATCTTGTAGATACGAGATGCTTCGCGGAATTTGTATACAGTGTCTCGATG 1046
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Db 998 CCAGGGAAGTTTTCAGAGATGAGATGTGCTTCGCGGAACCGTGGAGACAGTGTCTCGATG 1057
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QY 1047 GCTGTCTCAGCTCGTCTGTAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCTTTG 1106
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Db 1058 GCTGTCTCAGCTCGTCTGTAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCTTTG 1117
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QY 1107 TCCTTAGTTACGACATCTGGGTGGGAATCTTAGAGTACTGCCATGACAACTGGAG 1166
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QY 1167 GARGGCGGGGACGCTCAAGTCATCATGCGCTTACGCCAGGCTACACAGCTGTCTAC 1226
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Db 1178 GARGGTGGGATGAGCTCAAGTCATCATGCGCTTACGCCAGGCTACACAGCTGTCTAC 1237
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QY 1227 AATGGTAGTACAGAGGGGACGCTACACAGCATGTGTGCGGAATCTCAAAAGCTTATCG 1286
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Db 1238 AATGGCGATACAAAGAGAGAGCACTCGCGAGAGCAAGCGGACCTCATATAAGTGGCTCG 1297
QY 1287 TAGTCCAGATTGAGTCTGCACACTCGACTCCATGAGTAGTAGGATCGCTAGTAATCGCGGA 1346
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QY 1407 AGTTGATGACACAGAGTGGTTAGCTTAA-CTTAGTGAGGGGATGATCACCAGTGGT 1465
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QY 1466 CGATGACTGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1525
Db 1478 TCATGACTGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1537
QY 1526 C 1526
Db 1538 C 1538

RESULT 8
US-09-465-355-2
; Sequence 2, Application US/09465355
; Patent No. 6316194
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Knowles, David
; APPLICANT: Murchie, Alastair
; APPLICANT: Lentzen, Georg
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Antimicrobials
; FILE REFERENCE: 22620/1150 (Formerly 3950/85276)
; CURRENT APPLICATION NUMBER: US/09/465,355
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/325,601
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: GB 9812196.5
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: GB 9904790.4
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/122,439
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/088,241
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1542
; TYPE: RNA
; ORGANISM: Escherichia coli
US-09-465-355-2

Query Match 70.1%; Score 1069.2; DB 4; Length 1542;
Best Local Similarity 67.2%; Pred. No. 0;
Matches 1009; Conservative 247; Mismatches 241; Indels 4; Gaps 4;

QY 30 GCGCGAGGCTTAACATGCAAGTCGAGCGGGAAC-GATGATAGCTTGTATTAGCGGT 88
Db 38 GCGCGAGGCTTAACATGCAAGTCGAGCGGGAACGATGATAGCTTGTATTAGCGGT 97
QY 89 CGAGCGCGGAGCGGTGAGTAACTTCTAGGAATCTACCTAGTGTGGGGATAGCTCGG 148
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QY 149 GGAATCTGATTAATACCGAT-ACGCTACGGGGAAGAAAGAGGGGNTGATAGACTT 207
Db 158 GGAATCTGATTAATACCGAT-ACGCTACGGGGAAGAAAGAGGGGNTGATAGACTT 207
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Db 218 UUGCCAGUGGAGGCGGAGGAGUAGUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 277

QY 258 GACGATCTGTAGTGTCTGAGAGGATGATCAGCCACACCGGAGCTGAGACACGCGCCCGG 327
Db 278 GACGAUCCUUGGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 337
QY 328 ACT-CTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 386
Db 338 ACUCCUACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 397
QY 387 TGGCGCTGTGTGAAGAGGCGCTTTTGGTTGTAAAGCACTTTAAAGCACTTTAAAGCACT 446
Db 398 UGCGCGGUGUAGUAGAGAGGCGUUCGGGUGUAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 457
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Db 458 UAAAGUUAUACCUUUGGUGUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 517
QY 507 CCAGCAGCCGCGGTAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 566
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Db 638 UGAUACUGGCAAGCUGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 697
QY 687 GCGTAGAGATCTGAAGGAATACCGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 746
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QY 747 GAGCTCGAAGCGTGGGTAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 806
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QY 807 GATGCTACTAGTGTGTGGTCCCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 866
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      387 TCCCGCGTGTGTGAAGAAGGCCCTTTTGGTTGTAAAGCACCTTTAAGCAGTGAAGAAGATC 446
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      447 TTCGGTTAATACCCGGGGAGCATGACATTAGCTGCAGANAAGCACCGGCTAATCTCTG 506
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      507 CCAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTACTGGCGCTAAAGCG 566
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      567 AGCGTAGTGGCTTGATAGTACAGATGTGAATCCCGGGCTTAACCTGGGAACATGCATC 626
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      771189 CACGCGAGCGGTATTATTAAGTGAGGTGTGAAGCCCTGGGCTTAACCTAGGAATTGCATT 771248
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      627 TGAACCTGTAGGCTAGATAGTGGTAGAGGAGTGAATTTAGTGTAGCGGTGAAT 686
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      771249 TCAGACTGGTACTAGATAGTACTTTAGGAGGGGTAGAAATTCACGCTGAGCGGTAAAT 771308
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      687 GCGTAGATCTGAAGGAATACCGATGCGAAGGCGAGCTTCCTGGCATCATCTGACACT 746
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      771309 GCGTAGATCTGGAGGAATACCGAAGGCGAAGCGACGCCCTTGGGAATGACTGACGCT 771368
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      747 GAGGCTCGAAGCGTGGGTAGCAACAGGATTAGATACCTTGGTAGTCCACGCCGTAAAC 806
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      771369 CATGTGCGAAGCGTGGGAGCAACACAGGATTAGATACCTTGGTAGTCCACGCTGTAAC 771428
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      807 GATGCTACTAGTGTGGTCCCTTGAGAGCTTASTGACGAGCTAAGCGCAATAGTAG 866
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      771429 GCTGTCGATTTGGGGATTGGG--CTTAGAGCTTGTGCCCCCTAGCTAACGTGTAATCG 771486
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      867 ACCGCTGGGAGTACGCGCGCAAGGTAAAACTCAATGAATTTAGCGGGGCGCGCACA 926
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      771487 ACCGCTGGGAGTACGCGCGCAAGGTAAAACTCAATGAATTTAGCGGGGCGCGCACA 771546
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      927 AGCGGTGGAGCATGTGGTTAATTCGATCAACGCGGAAGACCTTACTCGTCTTGACAT 986
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      771547 AGCGGTGGAGCATGTGGTTAATTCGATCAACGCGGAAGACCTTACTCGTCTTGACAT 771606
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      987 ACACAGATCTGTAGAGATACGAGAGTGCCTTCGGGAATTTGTGATACAGTGTCTCATG 1046
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      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1047 GCTGTCGTCAGCTGCTGTCGATGATTTGGGTAAAGTCCCGCAACGAGCGCAACCCCTTG 1106
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      771667 GCTGTCGTCAGCTGCTGTCGATGATTTGGGTAAAGTCCCGCAACGAGCGCAACCCCTTG 771726
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      1107 TCCTTAGTTACCAGCACTTCGGTGGGAACTCTAAGGATATCTGCCAGTGAACAACTGGAG 1166
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      771727 TCCTTTTGTCCAGCAGCTTGTGGGAACTCAAAGGAGACTGCCAGTGAATAAATGGAG 771786
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      1167 GAGGCGGGGAGCAGCTCAAGTCAATCATGTCCTTACGACGAGGCTTACACAGCTGTCTAC 1226
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      771787 GAGGTGGGGATGACGTCAGTCAATCATGTCCTTACGAGTAGGGCTTACACAGCTGTCTAC 771846
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      1227 AATGTTAGTACAGAGGAGCTACACAGCATGTGATGCGGAATCTCAAAAGACCTTATCG 1286
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      771847 AATGCGGTATACAGAGGAGACGAGCTCGAGGTGGAGGAATCTCATTAAGTAGCTCT 771906
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATTCGCTAGTAAATCGCGA 1346
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      771907 AAGTCGGAATTGGAGTCTGCACTCGACTCCATGAAGTGGGAATTCGCTAGTAAATCGCGA 771966
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1347 TCAGAAATCCCGGTTGAATAGTTCCTGGGCGCTTTATACACACCGCGCTCACACCATGGG 1406
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      771967 TCAGAAATGTCGGGTGAATAGTTCCTGGGCGCTTTATACACACCGCGCTCACACCATGGG 772026
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Db 1534 CCTC 1537

RESULT 13

US-09-557-884-1

Sequence 1. Application US/09557884

Patent No. 6506581

GENERAL INFORMATION:

APPLICANT: Flietschmann et al.

TITLE OF INVENTION: The Nucleotide sequence of

the Haemophilus influenzae Rd Genome, Fragments

Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB186P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

Query Match 66.18; Score 1008.8; DB 4; Length 1830121;
 Best Local Similarity 81.68; Pred. No. 0;
 Matches 1225; Conservative 0; Mismatches 270; Indels 6; Gaps 5;

QY 30 GCGCGCAGGCTTAACACATCAAGTCCGAGCGAAAC-GATGATAGCTTGTCTATTAGGCGT 88
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 Db 770649 GCGCGCAGGCTTAACACATCAAGTCCGAGCGTACGAGGAASCTTGTCTTCTG 770708
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QY 89 CGAGCNGCGGACGGGTGAGTAATCTAGGAATCTACCTAGTAGTGGGGATAGCTCGG 148
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 770709 ACGAGTGGCGGACGGGTGAGTAATGCTTGGGAATCTGCTTATGAGGAGGAGTACGAGC 770768
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QY 149 GGAACACTGCAATTAATACCCATA-CGTCTACGGGAGAAACGAGGGGNTCATAGACCTT 207
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 Db 770769 GGAACACTGCAATTAATACCCGCTATTATCGGAAGATGAAGTGGGAGTACGAGGCGC 770828
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QY 208 GCGCTATTAGATGACCTTAAGTCGATAGTGTGGGTAAAGGCTTACCATGCG 267
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 Db 770829 ATGCCATAGTAGGCCCAAGTGGGATAGTGTGGGTGAATTCCTTACCAAGCC 770888
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QY 268 GACGATCTGTAGTGGTCTGAGAGGATGATCAGCCACACCGGACTGAGACAGCGCGG 327
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 Db 770889 TGGGATCTAGTGGTCTGAGAGGATGACCAACACACTGGAACACTGAGACAGGCTCCAG 770948
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Db 772027 AGTGGTGTACAGAGTAGATAGCTTACCTTTGGAGCGGTTTACCACGGTAGAT 772086
 QY 1466 CCATGACTGGGTGAAGTGTGAACAGGTAGCCGTAGGGGAACCTTGGGGTGGATCACCT 1525
 Db 772087 TCATGACTGGGTGAAGTGTGAACAGGTAGCCGTAGGGGAACCTTGGGGTGGATCACCT 772146
 QY 1526 C 1526
 Db 772147 C 772147
 RESULT 14
 US-09-557-884-1/c
 ; Sequence 1, Application US/09557884
 ; Patent No. 6506581
 ; GENERAL INFORMATION:
 ; APPLICANT: Fieischmann et al.
 ; TITLE OF INVENTION: The Nucleotide sequence of
 ; the Haemophilus influenzae Rd Genome, Fragments
 ; Thereof, and Uses Thereof
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3 1/2 inch diskette
 ; COMPUTER: Dell Pentium
 ; OPERATING SYSTEM: MS DOS v6.22
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/557,884
 ; FILING DATE: 25-Apr-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/476,102
 ; FILING DATE: JUN-5-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Michelle S. Marks
 ; REGISTRATION NUMBER: 41,971
 ; REFERENCE/DOCKET NUMBER: PB186P3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8439
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1830121 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-557-884-1

Query Match 66.18; Score 1008.8; DB 4; Length 1830121;
 Best Local Similarity 81.68; Pred. No. 0;
 Matches 1225; Conservative 0; Mismatches 270; Indels 6; Gaps 5;
 QY 30 GCGCGAGCGCTACACATGCAAGTCGAGCGGAAC-GATGATAGCTTCCATTAGCGCT 88
 Db 128085 GCGCGAGCGCTACACATGCAAGTCGAGCGGAAGCTTCTTCTTCTGCT 128026
 QY 89 CGAGNCGCGGAGCGGTGAGTATACCTTAGGAATCTACCTAGTAGTGGGGATAGCTCGG 148
 Db 128025 ACGAGTGGCGGACGCGGTGAGTATGCTTGGGAATCTGGCTTAGGAGGGGATACGCG 127966
 QY 149 GGAACCTGGAATTAACCGCATTA-CGTCTACGGGAGAAAGACGAGGNNCATATGACCTT 207
 Db 127965 GGAACCTGCGTAAATACCGCATTAATATCGGAAGATGAAAGTCGCGGACTGAGAGCGCG 127906

QY 208 GCCTATTATAGTAGCCTTAAGTCGGATTAGCTAGTGGTAAAGGCTTACCATGSC 267
 Db 127905 ATGCCATAGATGAGCCCAAGTGGATTAGGTGGTGGTAAATGCTTACCAGCC 127846
 QY 268 GAGCACTCTAGCTGGTCTGAGAGAGATGATCAGCCACACACCGGGACTGAGACACGGCCGG 327
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 QY 328 ACT-CTACGGGAGGAGCAGTGGGGAATATGGAACATGNGNGGAAACCTTGATCCAGCCA 386
 Db 127785 ACTCCTACGGGAGGAGCAGTGGGGAATATGCGCAATGGGGGGAACCTTGAGCGCAGCCA 127726
 QY 387 TGCCTGCTGTGTAAGAGCGCTTTTGGTTGTAAGACACTTTTAAGCAGTGAAGAAACTC 446
 Db 127725 TGCCTGCTGAATGAGAGAGCGCTTTCGGGTGTAAAGTCTTTCGGTATTGAGGAAGTTG 127666
 QY 447 TTCGGTTAATACCCGGGAGCAGTACATAGCTGAGAAATAGCACCAGCGCTAACTCTGTG 506
 Db 127665 ATGTGTAAATAGTACATCAAAATTCACGTAAATACAGAGAGAGCAGCGGCTAACTCCGTG 127606
 QY 507 CCAGCAGCGCGGTAAATACAGAGGTCAGAGCGTAAATCGGAATTAAGTGGCTTAAAGCG 566
 Db 127605 CCAGCAGCGCGGTAAATACAGAGGTCAGAGCGTAAATCGGAATTAAGTGGCTTAAAGCG 127546
 QY 567 AGCTAGTGGCTTGTATAGTCAAGTGAATTCCTCCGCGCTTAACTGGGAACTCATC 626
 Db 127545 CACGAGCGCGGTATTTAAGTGAAGTGTGAAGCGCTTAACTGGGAACTTTCATT 127486
 QY 627 TGAACCTGTAGCTAGTAGTAGTGAGAGGAGTAGATTTTCAGCTGTAGCGTGAAT 686
 Db 127485 TCAGACTGGGTAACTAGTAGTACTTTAGGGAGGGGTAGATTCACAGTGTAGCGGTGAAT 127426
 QY 687 CGCTAGAGATCTGAAGGAATACCGATCGGAGGAGGTCTCTGCGCATATACCTGACAT 746
 Db 127425 CGCTAGAGATGTGGAGGAATACCGAGCGGAGCGCCCTTGGGAATGTACTGACCT 127366
 QY 747 GAGCTCGAAAGCGTGGGTAGCAACAGGATTAGATCCCTGGTGTAGTCCACGCGCTAAC 806
 Db 127365 CATGTGCGAAAGCGTGGGAGCAACAGGATTAGATCCCTGGTGTAGTCCACGCTTAAAC 127306
 QY 807 GATGCTACTAGTGTGGTGGCTTGGAGCTTAGTGACGAGCTAGTGACGAGTAAAGTAG 866
 Db 127305 GCTGTGANTTGGGGANTGGG--CTTAGAGCTTGGTGGCCGTAGCTACGTGATTAATCG 127248
 QY 867 ACCGCTTGGGGAGTACGGCCGCAAGTTAAACTCAATGAAATGACGGGGGCGCCGACACA 926
 Db 127247 ACCGCTTGGGGAGTACGGCCGCAAGTTAAACTCAATGAAATGACGGGGGCGCCGACACA 127188
 QY 927 AGCGGTGAGCATGTGGTTAATTCGATGCAACGCGAAGAACCTTACTGTGCTTGACAT 986
 Db 127187 AGCGGTGAGCATGTGGTTAATTCGATGCAACGCGAAGAACCTTACTGTGCTTGACAT 127128
 QY 987 ACACAGAACTTTGTAGATACGAGAGTGCCTTTCGGGAATTTGTATACAGGTGCTGCATG 1046
 Db 127127 CCTAAGAAGAGCTPCAGAGATGAGCTTGTGCTTTCGGGAACCTTAGAGACAGGTGCTGATG 127068
 QY 1047 GCTGTCTGAGTCTGCTGAGATGTGGTTAAGTCCCGACGACGAGCGACACCTTGG 1106
 Db 127067 GCTGTCTGAGTCTGCTGAGATGTGGTTAAGTCCCGACGAGCGACACCTTGG 127008
 QY 1107 TCCTTAGTTACCAGCACTTGGGTGGGAACCTTAAGGATACCTCCAGTGAACAACTGGAG 1166
 Db 127007 TCCTTAGTTACCAGCACTTGGGTGGGAACCTTAAGGATACCTCCAGTGAACAACTGGAG 126948
 QY 1167 GAAGCGGGGAGCAGCTCAAGTCAATCATGCGCTTACGACCAGGGGTACACAGTGTCTAC 1226
 Db 126947 GAAGGTGGGGATGACGTCAAGTCAATCATGCGCTTACGAGTAGGGGTACACAGTGTCTAC 126888
 QY 1227 AATGTTAGTACAGAGGCGGAGTACACAGCGATGTGATCGGATCTCAAAAGCCCTATCG 1286
 Db 126887 AATGTTAGTACAGAGGCGGAGTACACAGCGATGTGATCGGATCTCAAAAGCCCTATCG 126828
 QY 1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATCAAGTAGGAACTCGCTAGTAACTCGCGGA 1346

Db 126827 AAGTCGGATGAGTGCACATCGACTCCATGACTCGAATCCCTAGTAATCGCAA 126768
QY 1347 TCAGAAATCCCGGCTGAATAGTCCCGGGCCCTGTGTACACACCGCCGCTCAACACATGGG 1406
Db 126767 TCAGAAATCCCGGCTGAATAGTCCCGGGCCCTGTGTACACACCGCCGCTCAACACATGGG 126708
QY 1407 AGTTGATTGCACAGAGTGGTGTAGCTAA-CTTAGTGAGGGCGATCACCGGTGTGGT 1465
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QY 1466 CGATGACTGGGCTGAAGTGTGTACAGAGTAGCGTAGGGGAACCTCGGCTGGATCACT 1525
Db 126647 TCATGACTGGGCTGAAGTGTGTACAGAGTAGCGTAGGGGAACCTCGGCTGGATCACT 126588
QY 1526 C 1526
Db 126587 C 126587

RESULT 15

US-09-643-990A-1

Sequence 1, Application US/09643990A

Patent No. 6528289

GENERAL INFORMATION:

APPLICANT: Robert D. Fleischmann

Mark D. Adams

Owen White

Hamilton O. Smith

J. Craig Venter

TITLE OF INVENTION: The Nucleotide sequence of

the Haemophilus influenzae Rd Genome, Fragments

thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESS: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville,

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A

FILING DATE: 23-Aug-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429

FILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787

FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PB186P1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-610-5790

TELEFAX: 310-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

Query Match

Best Local Similarity 66.1%; Score 1008.8; DB 4; Length 1830121;

81.6%; Pred. No. 0;

Matches 1225; Conservative 0; Mismatches 270; Indels 6; Gaps 5;

QY 30 GCGCGCAGGCTTAACACATCGAGCTCGAGCGGAAC-GATGATAGTCTTCTATTAGCGCT 88
Db 770649 GCGCGCAGGCTTAACACATCGAGCTCGAGCGGAACGCTTCTTTCTTCTGCTG 770708
QY 89 CGAGCNGCCGACGGGTGAGTATCTTAGNACTACCTAGTAGTGGGGGATACCTCGG 148
Db 770709 ACGATGCGCGACGGGTGAGTATCTTGGGAATCTGGCTTATGAGGGGGGATACGACG 770768
QY 149 GGAAGCTCGAATTAATACCCATA-CGCTACGGGGAAGACAGAGGAGGNTCATTAGACCTT 207
Db 770769 GGAAGCTCGCTTAATACCCGCTTATTCGGAAGATGAAGTGGGACTGAGAGGGCCG 770828
QY 208 GCGCTATTAGTAGAGCCCTAAGTCGGATTAGTAGTGGTGGGTAAAGCGCTACCATGGC 267
Db 770829 ATGCCATAGGATGAGCCCAAGTCGGATTAGTAGTGGTGGGTAAATGCTTACCAAGC 770888
QY 268 GACGATCTGAGTGGTCTGAGAGGATGATCAGCCACACCGGGAGTGAACAGCGCCCGG 327
Db 770889 TCGGATCTCTAGCTGGTCTGAGAGGATGACAGCCACACTGGAACTGAGACACGGTCCAG 770948
QY 328 ACT-CTACGGGAGCGACAGTGGGGAATATTGGACAATGGGGAACCGCTGATCAGACCA 386
Db 770949 ACTCTACGGGAGCGACAGTGGGGAATATTGGCAATGGGGAACCGCTGAGCGACCA 771008
QY 387 TCCCGCTGTGTGAAGAAGCCCTTTTGGTTGTAAAGCACTTAAAGCAGTGAAGAAGACTC 446
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QY 447 TFCGGTTAATACCGGGGAGATGACATTAAGTGCAGAAATAGCAGCGGCTAACTCTGTG 506
Db 771069 ATGCTTTAATAGTACATCAATTAAGCTTAATACAGAAAGACCGCGCTAACTCCGTG 771128
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QY 567 ACGGTAGTGGCTTGATAGTCAAGTGTGAATCCCGGGCTTAACTCGGAACTGCATC 626
Db 771189 CACGCGCGGCTTATTTAAGTAGGTGTGAAGCCCTTAACTAGGAATTCGAT 771248
QY 627 TCAGACTCTTAGCTAGCTAGTGTGAGAGGAGTGAATTCAGTGTAGCGGTGAAT 686
Db 771249 TCAGACTCTTAGCTAGCTAGTGTGAGAGGAGTGAATTCAGTGTAGCGGTGAAT 771308
QY 687 GCGTAGATCTGAAGGAATACCGATGCGAAGGAGCGCTTCCCTGGCATCATCTACACT 746
Db 771309 GCGTAGATCTGAGGAATACCGATGCGAAGGAGCGCTTCCCTGGCATCATCTACACT 771368
QY 747 GAGGCTCGAAGCGTGGGTAGCAACAGATTAATACCTGTGTAGTCCACGCCCTAAAC 806
Db 771369 CATGTGCGAAGCGTGGGAGCAACAGATTAATACCTGTGTAGTCCACGCCCTAAAC 771428
QY 807 GATGTCTACTAGTGTGGTCTCCCTTGAAGGACTTAGTGACGAGCTAAACGCAATAGTAG 866
Db 771429 GCTGTGCTTTGGGATGGG--CTTAGAGCTTGGTCCCGTAGCTAAGCTGATATATCG 771486
QY 867 ACCGCTGGGAGTACGGCGCAAGGTTAAACCAATGAATGACGGGGGCCGCGACA 926
Db 771487 ACCGCTGGGAGTACGGCGCAAGGTTAAACCAATGAATGACGGGGGCCGCGACA 771546
QY 927 ACGGTGAGCATGTGGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGTGTGTGACAT 986
Db 771547 ACGGTGAGCATGTGGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGTGTGTGACAT 771606
QY 987 ACACAGATCTTGTAGAGATACGAGTGCCTTCGGGAATGTGATACAGGTGTGATG 1046
Db 771607 CCTAAGAGAGCTCAGAGATGAGCTTGTGCTTCGGGAATGTGATACAGGTGTGATG 771666
QY 1047 GCTGTGCTGAGCTGT 1106
Db 771667 GCTGTGCTGAGCTGT 771726

Db 244 ACATCCGTAACCTGCTGAGAGGATGATCAGTCACTGGAACCTGAGACACGGTCCAGA 303
QY 329 CT-CTACGGAGGACAGTGGGCAATATTGGACAAATGGGGAACCTGATCCACCAT 387
Db 304 CTCTACGGAGGACAGTGGGCAATATTGGACAAATGGGGAAGCTGATCCACCAT 363
QY 388 GCGCGGTGTGAAGAAGCCCTTTTGGTTGTAAGCACTTTAAGCAGTGAAGAACTCT 447
Db 364 GCGCGGTGTGAAGAAGGCTTCGGATTGAAGCACTTTAAGTTGGGAGGAGGGCAT 423
QY 448 TCGGTTAATACCCGGGACAGTACATAGCTGCAGAAATAAGCAACCGGCTAACTCTCTGC 507
Db 424 TAACCTAATACCTTTAGTTTGTAGCTTACCGACAGAAATAAGCAACCGGCTAACTCTCTGC 483
QY 508 CAGCAGCCGCTAATACAGAGGTCGACAGCTTAACTGGAATTAAGTGGGCGTAAAGCA 567
Db 484 CAGCAGCCGCTAATACAGAGGTCGACAGCTTAACTGGAATTAAGTGGGCGTAAAGCG 543
QY 568 GCGTAGGTGCTGTGATAAGTCAAGTGTGAATCCCGGGCTTAACCTGGGAACCTGATCT 627
Db 544 GCGTAGGTGCTGTGATAAGTGTGAATCCCGGGCTTAACCTGGGAACCTGATCTCTGC 603
QY 628 GAACTGTAGCTAGCTAGGTGAGAGGAAGTAGAATTTAGGTGAGGTGAGGAATG 687
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QY 688 CFTAGAGATCTGAAGGATACCGATGCCGAGGACAGCTTCCTGGCATCACTGACATG 747
Db 664 CFTAGATATAGGAAGGACACAGTGGCGAAGGACACACCTGGACATGACTGACATG 723
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Db 724 AGGTGCGAAGCGTGGGAGGCAACACAGATTAGTACCTGGTAGTCCAGCGCGTAAAG 783
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QY 928 GCGGTGAGCATGTGTTTAAATTCGATGCAACGCAAGAAACCTTACCTGTGTGTGACATA 987
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QY 988 CACAGATCTTGTAGATACAGAGTGCCTTCGGGAATTTGATACAGGTGTGATG 1047
Db 964 CAATGAACCTTCCAGAGATGGATGGTGGCTTCGGGAACATTGAGACAGGTGTGATG 1023
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Db 1084 CTTTGTATCCAGACACATATGTTGGCACTCTTAAGGAGCTGCGGTGACAAACCGGAG 1143
QY 1167 GAAGGGGGGACGCTCAAGTCAATCATGTCCTTACGACAGGCTTACACAGTGTCTAC 1226
Db 1144 GAAGGTGGGGATGAGCTCAAGTCAATCATGTCCTTACGACGCTGGGCTTACACAGTGTCTAC 1203
QY 1227 AATGTTAGGTACAGAGGACGTACACAGGATGTGATCGAATCTCAAAAGGCTATCG 1286
Db 1204 AATGTTAGGTACAGAGGTTGCCAAGCCGAGGTGGAGCTTAATCCCAAAACCGATCG 1263
QY 1287 TAGTCCAGATTTGAGTCTGCAACTCGACTCCATCCATGAAGTAGGAAATCGTAAATTCGCGGA 1346
Db 1264 TAGTCCGATTTGAGTCTGCAACTCGACTCCGTTGAAGTGGAAATCGTAAATTCGCGGA 1323
QY 1347 TCAGATTCGGGGTGAATAGTTCGCGGGCTTTGTACACACCGCGCTTACACCATGGG 1406

Db 1324 TCAGAAATGTGCGGGTGAATAAGTTTCCGGGCTTGTACACACCGCGCTCACACCATGGG 1383
QY 1407 AGTTGATTGCACACAGAACTGTTAGCCTAA-CTTAGTGAAGGCGGATCACACAGGTGTGCT 1465
Db 1384 AGTGGTTGCACACAGAACTAGTCTAAGCTTGGGAGGACGGTTACACCGGTGTGAT 1443
QY 1466 CGATGACTGCGGTGAAGTCTGTAACAGGTAGCCGTAGGGGAACCTGGGCTGTGATCAC 1523
Db 1444 TCATGACTGGGTGAAGTCTGTAACAGGTAGCCGTAGGGGAACCTGGGCTGTGATCAC 1501

RESULT 2
US-09-745-476-1
; Sequence 1, Application US/09745476
; Patent No. US20010029039A1
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09/745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 1501
; ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-09-745-476-1

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;
Best Local Similarity 85.9%; Pred. No. 2.3e-289;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGGCGAGCGTTAAACATGCAAGTCGAGCGGAAAGATGATGCTTATTTAGCGGTC 89
Db 9 GCGGCGAGCGCTAAACATGCAAGTCGAGCGG--ATGACGGGAGGCTTCTCTGAATCA 66
QY 90 GAGGCGCGGAGCGGTGAGTAACTATTAGGAATCTACCTAGTGTAGTGGGAGTACTCGGG 149
Db 67 G---CGGCGGAGCGGTGAGTAACTGCTTAGGAATCTGCTTGGTGGGACACGCTC 123
QY 150 GAAACTCGAATTAATPACCGCATACGT-CTACGGGAGAAAGACAGGGGNTCAATAGACCTG 208
Db 124 GAAAGGAGCGCTAATACCGCATACGTCTACGGGAGAAAGACAGGGGACCTTCGGGCGCTG 183
QY 209 CGCTATTAGATGAGCTTAACTGCGATTTAGCTAGATGGTGGGTAAAGCCCTACCATGGCG 268
Db 184 CGCTATCAGATGAGCTTAACTGCGATTTAGCTAGTGGTGGTAAATGCTCAACAGGCG 243
QY 269 ACATCTGTAGCTGCTCTGAGAGGATGATCAGCCACACCGGACTGAGACACGCGCGGA 328
Db 244 ACATCGTAATCTGCTCTGAGAGGATGATCAGTCACTGGAATGAGACAGCTCCAGA 303
QY 329 CT-CTACGGGAGGACAGTGGGGAATTTGGAATATGNGGGAACCCCTGATCCAGCAT 387
Db 304 CTCTACGGGAGGACAGTGGGGAATTTGGAATATGNGGGAACCCCTGATCCAGCAT 363
QY 388 GCGCGGTGTGAAGAAGCCCTTTTGGTTGTAAGCACTTTAAGCAGTGAAGAACTCT 447
Db 364 GCGCGGTGTGAAGAAGGCTTTCGATTTGAAGCACTTTAAGTTGGGAGGAGGCGAT 423
QY 448 TCGGTTAATACCCGGGACGATGATGATGCTGAGAAATAAGCAACCGGCTAACTCTGTGC 507
Db 424 TAACCTAATACCTTTAGTTTGTAGCTTACCGACAGAAATGAGCCGCTAATCTGTGC 483
QY 508 CAGCAGCCGCTAATACAGAGGTCGACAGGTTAATCGGAATTAAGTGGGCGTAAAGCA 567
Db 484 CAGCAGCCGCTAATACAGAGGTCGACAGGTTAATCGGAATTAAGTGGGCGTAAAGCG 543
QY 568 GCGTAGGTGCTGTGATAAGTCAAGTGTGAATCCCGGGCTTAACTGGGAACCTGATCT 627
Db 544 GCGTAGGTGCTGTGATAAGTGTGAATCCCGGGCTTAACTGGGAACCTGATCTCTC 603

Db 904 GCGGTGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACTTACCAGGCGTTGCATC 963
QY 988 CACAGATCTTTAGAGATACAGAGTGCCTTCGGGAATTTGATACAGGTGTCGATGG 1047
Db 964 CAATGAACATTTCCAGAGATGATGGGTGCCTTCGGGAACATTTGACAGAGTGTGTCATGG 1023
QY 1048 CTGTCGTGAGCTGCTGCTGAGATGTTGGTTAACTCCGCAACGAGCGCAACCTTGT 1107
Db 1024 CTGTCGTGAGCTGCTGCTGAGATGTTGGTTAACTCCGCAACGAGCGCAACCTTGT 1083
QY 1108 CTTTGTATCCAGACAC-TTCGGGTGGGAATCTTAAGATACCTGACAGTGCATGAG 1166
Db 1084 CTTTGTATCCAGACAC-TTCGGGTGGGAATCTTAAGATACCTGACAGTGCATGAG 1143
QY 1167 GAAGCGGGGAGAGCTGATCATCATGCTTACGCTTACGAGCGGTACACAGTGCATC 1226
Db 1144 GAAGGTGGGATGACGTCAATCATCATGCTTACGCTTACGAGCGGTACACAGTGCATC 1203
QY 1227 AATGGTAGGTACAGAGGCGACTACAGCGATGTGATCGAATCTCAAAAAGCCTATCG 1286
Db 1204 AATGGTAGGTACAGAGGCGACTACAGCGATGTGATCGAATCTCAAAAAGCCTATCG 1263
QY 1287 TAGTCCAGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1346
Db 1264 TAGTCCGAGTTCGACGCTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
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Db 1324 TCAGATGCTGCGGTGATACGATGTTCCCGGCTTGTACACACCGCGCTGACACCATGG 1383
QY 1407 AGTTGATTCACACAGATGTTAGCCTAA-CTTAGTGGGCGGCTACACACCGGTGTGT 1465
Db 1384 AGTGGGTGACACAGATGCTAGTCTAACCCTTCGGGAGGAGGCTTACACCGGTGTAT 1443
QY 1466 CGATGCTGGGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1523
Db 1444 TCAGTACTGGGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1501

RESULT 4
US-09-748-205-1
; Sequence 1, Application US/09748205
; Patent No. US2002022253A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate its manufacturing method, and microorganism
; FILE OF INVENTION: those are used for the method.
; FILE REFERENCE: 4351009
; CURRENT APPLICATION NUMBER: US/09/748,205
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-748-205-1

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;
Best Local Similarity 85.9%; Pred. No. 2.3e-289;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GGGGCGAGGCTTAACATATGATGCTGAGCGGAAACATGATGATGCTGCTTATGAGCGTC 89
Db 9 GGGGCGAGGCTTAACATATGATGCTGAGCGG--ATGAGCGGAGCTTCTCTCTGAATTC 66
QY 90 GAGCGCGGAGCGGTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 149
Db 67 G---CGGCGGAGCGGTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 123
QY 150 GAAACTCGAATTAATACCGCTAGCT-CTACGGGAGAAAGCAGGGGNTCTATTAGACCTTC 208
Db 124 GAAGGAGCGCTAATACCGCTAGCTCTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTCG 183

QY 209 GCGTATTAGATGAGCGCTAAGTCGGATTAGTAGTGGTGGCTTAAGCGCTTACCAGCGG 268
Db 194 GCGTATTAGATGAGCGCTAAGTCGGATTAGTAGTGGTGGCTTAAGCGCTTACCAGCGG 243
QY 269 ACGATCTGTAGTGGTCTGAGAGGATGATCAGCGACACCGCGGACTGAGACAGCGCGCGGA 328
Db 244 ACGATCGTAACTGGTCTGAGAGGATGATCAGTCACTGGAACCTGAGACAGCGTCCAGA 303
QY 329 CT-CTACGGGAGCGAGCTAGTGGGGAATATTGGCAATATGNGNGGGAACCTGATCCAGCAT 387
Db 304 CTCCTACGGGAGCGAGCTAGTGGGGAATATTGGCAATATGNGNGGGAACCTGATCCAGCAT 363
QY 368 GCGCGGTGTGTAAGAAGCGCTTTTGGTGTAAAGCACCTTTAAGCAGTGAAGAGACTCT 447
Db 364 GCGCGGTGTGTAAGAAGCGCTTTTGGTGTAAAGCACCTTTAAGCAGTGAAGAGACTCT 423
QY 448 TCGGTTAATACCGCGGAGCGATGACATTAGCTCAGAAATAGCACCGGCTAATCTGTGTGC 507
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QY 508 CAGCAGCGCGGTATATACAGAGGTGCAAGCGTTAATTCGGAATTTACTGGGCGTAAGCGA 567
Db 484 CAGCAGCGCGGTATATACAGAGGTGCAAGCGTTAATTCGGAATTTACTGGGCGTAAGCGG 543
QY 568 GCGTAGTGGCTGTGATAAGTCAGATGTGAATCCCGGCTTAACTGGGAACTGCATCT 627
Db 544 GCGTAGTGGTGTGATAAGTCAGATGTGAATCCCGGCTTAACTGGGAACTGCATCT 603
QY 628 GAAACTGTAGGCTAGTGTGAGAGGGAAGTAGAATTTCAAGTGTAGCGGTGAAATG 687
Db 604 AAAACTGACAAGCTAGATGATGAGAGGTGTTGGAATTTCTGTTAGCGGTGAAATG 663
QY 688 CGTAGAGTCTGAAGATACGATGCGGAGGAGCGACTTCTTGGCATCATACTACAGACTG 747
Db 664 CGTAGATATAGAGAGGAGACCCAGTGGGAGGCGACCTGGGACTGATACTGACACTG 723
QY 748 AGGCTGAAAGCGTGGGTAGCAAAACAGGATTAGATACCTGGTAGTCCACCGCTTAAAG 807
Db 724 AGGTGCGAAAGCGTGGGAGCAAAACAGGATTAGATACCTGGTAGTCCACCGCTTAAAG 783
QY 808 ATGCTACTAGTGTGTTGGTCCCTTGGAGGCTTGTAGTGGAGCTTAACGCAATTAAGTAG 867
Db 784 ATGTAACCTAGCGTGGGAGCGCTTGTAGTGGGCGAGCTTAACGCAATTAAGTAG 843
QY 868 CCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATTTGACGGGCGCGCGACAA 927
Db 844 CCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATTTGACGGGCGCGCGACAA 903
QY 928 GCGGTGAGCATGTGGTGTAAATTCATGCAACGCGAAGAACCTTACCTGTGCTTGAACATA 987
Db 904 GCGGTGAGCATGTGGTGTAAATTCATGCAACGCGAAGAACCTTACCAGGCTTGAACATC 963
QY 988 CACAGATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTTGTATACAGTGTGCTGATGG 1047
Db 964 CAATGAACCTTTCAGAGATGATGGGTGCCTTCGGGAATTTGTATACAGTGTGCTGATGG 1023
QY 1048 CTGTCGTGAGCTGCTGCTGAGATGTTGGTTAACTCCGCAACGAGCGCAACCTTGT 1107
Db 1024 CTGTCGTGAGCTGCTGCTGAGATGTTGGTTAACTCCGCAACGAGCGCAACCTTGT 1083
QY 1108 CTTTGTATCCAGACAC-TTCGGGTGGGAATCTTAAGATACCTGACAGTGCATGAG 1166
Db 1084 CTTTGTATCCAGACAC-TTCGGGTGGGAATCTTAAGATACCTGACAGTGCATGAG 1143
QY 1167 GAAGCGGGGAGCGCTAAGTCAATCATGCTTACGAGCGGTACACAGTGCATGAG 1226
Db 1144 GAAGGTGGGATGAGCTCAATCATCATGCTTACGCTTACGAGCGGTACACAGTGCATG 1203
QY 1227 AATGGTAGGTACAGAGGCGACTACAGCGATGTGATCGAATCTCAAAAAGCCTATCG 1286
Db 1204 AATGGTAGGTACAGAGGCGACTACAGCGATGTGATCGAATCTCAAAAAGCCTATCG 1263
QY 1287 TAGTCCAGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1346

1264 TAGTCCGATCGCAGTCTGCACTCGACTGCGTGAAGTCGGATCTAGTATCGCGAA 1323
1347 TCAGATCCCGCGTGAATAGTTCGCGGCGCTTGTCACACCGCCGCTCACACCATGG 1406
1324 TCAGATTCGCGGTGAATAGTTCGCGGCGCTTGTCACACCGCCGCTCACACCATGG 1383
1407 AGTTGATGACACCAAGTGGTTCAGCTAA-CTTAGTAGAGGGGATCACACCGGTGGT 1465
1384 AGTGGTTGCACAGATAGTCTAGTCTAACCTTCGGGAGAGCGTTACACCGTGGAT 1443
1466 CGATGACGCGGTGAATGCTGACAGGTAGCCGATAGCGGGAACCTCGCGTGGATC 1523
1444 TCATGACTGGGTGAATGCTGACAGGTAGCCGATAGCGGGAACCTCGCGTGGATC 1501

RESULT 5
US-09-793-920A-1
; Sequence 1, Application US/09793920A
; Patent No. US20020065389A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanoic acid as
; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/793,920A
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-793-920A-1

Query Match 72.08; Score 1098.6; DB 9; Length 1501;
Best Local Similarity 85.98; Pred. No. 2.3e-289;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGACGCTTACACATGCAAGTCGAGCGGGAACGATGATAGCTGCTATTAGCGTC 89
DB 9 GCGCGACGCTTACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCTGATTC 66
QY 90 GAGCNGCGGACGCGGTGAGTAACTTAGGAATCTACTAGTAGTGGGGATAGCTCGG 149
DB 67 G---CGGCGGACGCGGTGAGTAACTTAGGAATCTGCTGAGTGGGGACACAGCTC 123
QY 150 GAACTCGAATTAATACCGATACGT-CTACGGGGAAGAACGAGGNGTCAATAGACCTG 208
DB 124 GAAAGGACGCTTAATACCGATACGTCTCTACGGGGAAGAACGAGGACCTTCGGGCT 183
QY 209 CGCTATTAGATGACCTTAAGTCGATGATAGCTAGTGGGTAAAGGCTTACCATGCG 268
DB 184 CGCTATGATGACCTTAAGTCGATGATGATGATGATGATGATGATGATGATGATGAT 243
QY 269 AGATCTGATGCTGCTGAGAGGATGATGACGACACCGGAGTACGACACGCGCCGGA 328
DB 244 AGATCCGCTACTGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 303
QY 329 CT-CTACGGGAGGACGAGTGGGGAATATGGAATATGGAATATGGAATATGGAAT 387
DB 304 CTCCTTACGGGAGGACGAGTGGGGAATATGGAATATGGAATATGGAATATGGAAT 363
QY 388 GCGCGCTGTCGAGAGGCGCTTTGGTTGTAAGGACCTTAAAGCCTTAAAGCCTTAA 447
DB 364 GCGCGCTGTCGAGAGGCGCTTTGGTTGTAAGGACCTTAAAGCCTTAAAGCCTTAA 423
QY 448 TCGGTAAATACCCGGGACGATGATGATGATGATGATGATGATGATGATGATGATG 507
DB 424 TAACTTATAGTGTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 483
QY 508 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTAAATCGGAATTAATCGGAATTA 567
DB 484 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTAAATCGGAATTAATCGGAATTA 543

QY 568 GGTAGCTGCTTCTATAGTCAGATCTGAATCCCGGCTTAACTTGGGAACTGCACT 627
DB 544 GGTAGCTGCTTCTATAGTCAGATCTGAATCCCGGCTTAACTTGGGAACTGCACT 603
QY 628 GAACTGTTAGCTTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 687
DB 604 ARACTGACAGCTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 663
QY 688 CTTAGAGATCTGAAGGAATACCGATGGGAGGAGCTTCTTGGCATCATATGACACT 747
DB 664 CTTAGATATAGGAAGAACACAGTGGGAGGAGCTTCTTGGCATCATATGACACT 723
QY 748 AGCTCGAAGCGTGGGTAGCAACAGGATAGTATACCTGCTAGTCCAGCGCTAAAG 807
DB 724 AGTGGGAAGCGTGGGAGCAACAGGATAGTATACCTGCTAGTCCAGCGCTAAAG 783
QY 808 ATGCTACTAGTCTGTTGGTCCCTTGGAGACTTATGACGAGCTAACGCAATAGT 867
DB 784 ATGCTACTAGTCTGTTGGTCCCTTGGAGACTTATGACGAGCTAACGCAATAGT 843
QY 868 CGCTGCGGAGTACGCGCCCAAGGTTAACTCAATGAATGACGCGGCGCCGCAAA 927
DB 844 CGCTGCGGAGTACGCGCCCAAGGTTAACTCAATGAATGACGCGGCGCCGCAAA 903
QY 928 GCGTGGAGCATGTGTTTAACTTCGATGCAACGCGAGAACCTTACCTGCTTGCATA 987
DB 904 GCGTGGAGCATGTGTTTAACTTCGAGCAACGCGAGAACCTTACCGGCTTGCATC 963
QY 988 CACAGAATCTTGTAGATACGAGTGCCTTTCGGGAATTTGTATACAGTGTGCTATG 1047
DB 964 CAATGAATCTTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1023
QY 1048 CTGCTGCTAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1107
DB 1024 CTGCTGCTAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1083
QY 1108 CTTAGTTACCAAGCAGCTTTCGGGTGGAACTCTAAGGAGTCTCCAGTACAACTGG 1166
DB 1084 CTTAGTTACCAAGCAGCTTTCGGGTGGAACTCTAAGGAGTCTCCAGTACAACTGG 1143
QY 1167 GAAGCGGCGGACGCTTCAAGTCTCATGCGCTTTCAGCAGGCTTACACAGCTGCTAC 1226
DB 1144 GAAGTGGGATGAGCTCAAGTCTCATGCGCTTTCAGCAGGCTTACACAGCTGCTAC 1203
QY 1227 AATGTTAGTACAGAGGCGAGCTTACAGAGTGTATGGAATCTCAAAAGCTATGCT 1286
DB 1204 AATGTTAGTACAGAGGCGAGCTTCCCAAGCGGAGTGGAGCTTAATCCCAAAA 1263
QY 1287 TAGTCCAGATTGGAGTCTGCAACTTCGACTTCCAGTGAAGTGAAGTGAAGTGA 1346
DB 1264 TAGTCCAGATTGGAGTCTGCAACTTCGACTTCCAGTGAAGTGAAGTGAAGTGA 1323
QY 1347 TCAGAATCCCGGCTGAATACGTTCCCGGCGCTTGTACACACCGCGCTCACACCATGG 1406
DB 1324 TCAGAATCCCGGCTGAATACGTTCCCGGCGCTTGTACACACCGCGCTCACACCATGG 1383
QY 1407 AGTGTATGCAACAGAGTGTGTTAGCTTAA-CTTAGTGGGCGGATCACACCGGTGGT 1465
DB 1384 AGTGTATGCAACAGAGTGTGTTAGCTTAA-CTTAGTGGGCGGATCACACCGGTGGT 1443
QY 1466 CGATGACTGGGTGAAGTCTGCTTACAGAGTGGGTAGGGAACCTCGGCTGGATC 1523
DB 1444 TCATGACTGGGTGAAGTCTGCTTACAGAGTGGGTAGGGAACCTCGGCTGGATC 1501

RESULT 6
US-09-951-720-1
; Sequence 1, Application US/09951720
; Patent No. US20020160467A1
; GENERAL INFORMATION:
; APPLICANT: Canon Kabushiki Kaisha
; TITLE OF INVENTION: Polyhydroxyalkanoate and Manufacturing Method Thereof

FILE REFERENCE: 4477001
CURRENT APPLICATION NUMBER: US/09/951,720
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: JP 279900/2000
JP 378827/2000
JP 165238/2001
JP 165509/2001
JP 275063/2001
PRIOR FILING DATE: 2000-09-14
2000-12-13
2001-05-31
2001-05-31
2001-09-11
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii 161 strain.
US-09-951-720-1

Query Match
Best Local Similarity 85.9%; Pred. No. 2.3e-289;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGAGCTTACACATGCAAGTCGAGCGGAGAACATGATAGCTTCTATTAGGCGTC 89
D 9 GCGCGAGCGCTTACACATGCAAGTCGAGCGG--ATGACGGAGCTTGTCTCTGAATCA 66
QY 90 GAGCGCGGAGCGGCTGAGTAACTACTTAGGAACTACTAGTAGTGGGGATAGTCGCG 149
D 67 G--CGCGGAGCGGCTGAGTAACTGCTAGGAACTGCTGCTAGTGGGGAGCAACGCTC 123
QY 150 GAACTCGAATTAATACCGCATAGT-CTACGGGAGAAACGAGGNGNCTATTACCTTG 208
D 124 GAAGGGAGCGCTAATACCGCATAGTCTTACGGGAGAAACGAGGAGACCTTGGGGCGCT 183
QY 209 CGCTATTAGTAGAGCTTAAGTGGATAGTAGTAGTGGGGTAAAGGCGCTACCATGGCG 268
D 184 CGCTATCAGATGAGCTTGTGAGTGTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 243
QY 269 AGATCTAGCTGCTGAGAGGATGATCAGCACACCGGGAGTACAGACAGCGCGCGGA 328
D 244 AGATCCGCTAAGCTGAGAGGATGATCAGCACACCGGGAGTACAGACAGCGCGCGGA 303
QY 329 CT-CTACGGGAGCGAGTGGGGAATATTGGAATGNGGGAACCCCTGATPCCAGCAT 387
D 304 CTCCTACGGGAGCGAGTGGGGAATATTGGAATGNGGGAACCCCTGATPCCAGCAT 363
QY 388 GCGCGTGTGGAAGAGCGCTTTTGGTTGTAAGCACTTTAAGCACTTTAAGCACTTTAAG 447
D 364 GCGCGTGTGGAAGAGCGCTTTTGGTTGTAAGCACTTTAAGCACTTTAAGCACTTTAAG 423
QY 448 TCGGTTATACCGGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507
D 424 TACCTATAGCTTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 483
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D 484 CAGCAGCGCGCTAATACAGAGGCTGCAAGCTTAAATCGGAATTAATCGGAATTAATCG 543
QY 568 GCGTAGTGGCTTGTATAGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 627
D 544 GCGTAGTGGCTTGTATAGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 603
QY 628 GAACTGTGTAGCTAGTGTGAGAGGAGTGTGATGATGATGATGATGATGATGATGATG 687
D 604 ARACTGACAGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 663
QY 688 CGTAGAGTCTGAAGGAATACCGATGCGGAGGAGCTTCTTGGCATCATCTAGTACACTG 747
D 664 CGTAGATATAGGAAGAACACAGTGGCGAAGGCGACCACTGAGTGTGATGATGATGATG 723
QY 748 AGGCTCGAAGCGGTGAGTGAACAAACAGATTTAGATPACCTGTGTAGTCCAGCGCGTAA 807

Db 724 AGTTCGCAAGCGTGGGAGCAACACAGATTAGATACCTGTGTAGTCCACCGCGTAAAG 783
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QY 868 CCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGAATGACGGGGCGCGCACAA 927
Db 844 CCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGCGCGCACAA 903
QY 928 GCGGTGAGCATGTTGTTAATTCGATGCAAGCGGAGAACCTTACCTGTCTTGTGACATA 987
Db 904 GCGGTGAGCATGTTGTTAATTCGATGCAAGCGGAGAACCTTACCTGTCTTGTGACATA 963
QY 988 CACAGATCTTGTAGATACGAGAGTGCCTTCGGGAATTTGTATACAGTGTGTGATGCG 1047
Db 964 CAATGACATTCAGAGATGGATGGTGCCTTCGGGAACATTTAGACAGTGTGTGATGCG 1023
QY 1048 CTGTCTAGCTGTGTGTGATGTTGGTTAAGTCCCGCAGGAGCGACACCTTGT 1107
Db 1024 CTGTCTAGCTGTGTGTGATGTTGGTTAAGTCCCGCAGGAGCGACACCTTGT 1083
QY 1108 CTTTGTATACAGCAC-TTCGGGTGGGAATCTTAAGGATACTTGCAGTACAAACTGGAG 1166
Db 1084 CTTTGTATACAGCACGTAATGTTGGCACTCTTAAGGAGACTTGCAGTACAAACTGGAG 1143
QY 1167 GAAGCGGGAGCAGCTCAAGTCAATCATGTCCTTACGACAGGCTTACACAGTGTGTAC 1226
Db 1144 GAAGTGGGATGAGCTCAAGTCAATCATGTCCTTACGCTTGGGCTTACAGCTGTCTAC 1203
QY 1227 AATGTTAGTACAGAGGCGAGTACAGAGTGTGATGATGATGATGATGATGATGATG 1286
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QY 1287 TAGTCCAGATGGAGTCTCAACTCGACTCCATCAAGTGAAGTGAAGTGAAGTGAAGTGA 1346
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QY 1407 AGTTGATTACACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1465
Db 1384 AGTGGTGTGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1443
QY 1466 CGATGACTGGGTGAAGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1523
Db 1444 TCATGACTGGGTGAAGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1501

RESULT 7

US-791-610-1
; Sequence 1, Application US/09791610
; Publication No. US20030100084A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylalkanoic acid
; FILE REFERENCE: 4396021
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-791-610-1

Query Match 72.0%; Score 1098.6; DB 11; Length 1501;
Best Local Similarity 85.9%; Pred. No. 2.3e-289;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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QY 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
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Db 124 GAAAGGACGCTAATACCCATACGTCTACGGGAGAAACGAGGAGCTTCGGGCGCTTG 183
QY 209 CGCTATTAGATGAGCCTAAGTCGGAATAGCTAGATGCTGGGTAAGAGCCTACCATGGG 268
Db 184 CGCTATCAGATGAGCCTAGCTCGGATTAGCTAGTGGTGAATAGGCTACCAAGGCG 243
QY 269 ACGATCTGTAGCTGCTGAGAGGATGATCAGCCACACCGGAGCTGAGACAGCGGCCGGA 328
Db 244 ACGATCCGTAACTGCTGAGAGGATGATCAGTCACACTGGAAGTGAAGACAGCGTCCAGA 303
QY 329 CT-CTACGGAGGACAGTGGGGAATATTGGACAATGNGNGGAACCTGATFCAGGCAT 387
Db 304 CTCCTAGGGAGGACAGTGGGGAATATTGGACAATGNGNGGAACCTGATFCAGGCAT 363
QY 388 GCCCGCTGTGGAAGAGCGCTTTGGTTGTAAGACACTTATAGCAGTGAAGAGACTCT 447
Db 364 GCCCGCTGTGGAAGAGCGCTTCGGATTGTAAGACACTTATAGTGGGAGGAGGCGAT 423
QY 448 TCGGTTAATACCGGGGAGCATGACATTAGCTGCAGAAATAGCACCGGCTAACTGTGTC 507
Db 424 TAACCTAATACGTTAGTGTGTTGAGCTTACCGACAGAAATAGCACCGGCTAACTGTGTC 483
QY 508 CAGCAGCGCGGTAAATACAGAGGTCGAAGGTTAATCGGAATTAAGTCTGGGCTAAAGGA 567
Db 484 CAGCAGCGCGGTAAATACAGAGGTCGAAGGTTAATCGGAATTAAGTCTGGGCTAAAGGC 543
QY 568 GGGTAGGTGGCTGTAAGTCAAGTGTGAATATCCCGGCTTAACCTGGGAGTCACTCT 627
Db 544 GGGTAGGTGGCTGTAAGTGTGAATGTGAAGAGCGGCTCAACCTGGGAGTCACTCT 603
QY 628 GAACTGTAGCTAGTGTAGTGAAGGAGTAGAATTTACAGTGTAGCGGTGAATG 687
Db 604 AAACTCAAGCTAGATGATGTAAGGAGTGTGAATTTCTGTTAGCGGTGAATG 663
QY 688 CBTAGAGTCTGAAGAAATACGATCGGAGGAGGAGCTTCTGGCATCATCTGACACTG 747
Db 664 CBTAGATATAGGAAGAACACACAGTGGCGAAGGCGACCTGGAGTGAATCTGACACTG 723
QY 748 AGGCTGAAAGCGTGGGTAGCAAAACAGGATTAGATACCTGGTAGTCCACGCGCTAAACG 807
Db 724 AGGCTGAAAGCGTGGGAGCAAAACAGGATTAGATACCTGGTAGTCCACGCGCTAAACG 783
QY 808 ATGTCTACTAGTCTGGGTTCCTTGAGGACTTGTAGCAGCTAGTAAACCAATAGTAGA 867
Db 784 ATGTCAACTAGCCTTGGGAGCTTGAGCTCTTAGTGGCGCAGCTAAACCAATAGTAGA 843
QY 868 CCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATGACGGGGGCGCCGACAA 927
Db 844 CCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATGACGGGGGCGCCGACAA 903
QY 928 GCGGTGAGAGTGTGTTAATTCGATCAAGCGGAAGAACCTTACCTGGTCTTTCACATA 987
Db 904 GCGGTGAGAGTGTGTTAATTCGACAGCGGAGAACCTTACCGGCTTTCACATC 963
QY 988 CACAGAATCTTGTAGAGATACGAGATGCTCTCGGGAATTTGTATACAGGTGCTGCATGG 1047
Db 964 CAATCAACTTTCAGAGATGATGGTGGTTCCTTCGGGAACATTCAGACAGGTGCTGCATGG 1023
QY 1048 CTGTCTCAGCTCTGTGAGATGTTGGGTTAAGTCCCGCAACAGAGCGCAACCCCTGT 1107
Db 1024 CTGTCTCAGCTCTGTGAGATGTTGGGTTAAGTCCCGCAACAGAGCGCAACCCCTGT 1083
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QY 1108 CTTTAGTTACCAGCAC-TTCGGTGGGAACCTCTAAGGATACTCCAGTGCACAACTGGAG 1166
Db 1084 CTTTAGTTACCAGCACGTAATGTTGGGACACTCTAAGGAGACTCCCGGTTGACAAACCGGAG 1143
QY 1167 GAAGCGGGGAGACAGCTCAAGTCATCATGCGCCCTTAGCACCAGGCTACACACGTGCTAC 1226
Db 1144 GAAGTGGGATGACCTCAAGTCATCATGCGCCCTTAGCACCAGGCTACACACGTGCTAC 1203
QY 1227 AATGTAGGTACAGAGGCGAGCTACACAGCGATGTGATCGAATCTCAAAAAGCCTATCG 1286
Db 1204 AATGTGTGTACAGAGGTTGCCAAGCGGAGGTGAGCTAATCCCAAAACCGATCG 1263
QY 1287 TAGTCCAGATTGGAGTCTGCACTCGACTTCCAACTGAAGTAGGAATCTAGTAACTCGCGGA 1346
Db 1264 TAGTCCGATCGAGTCTGCACTCGACTCGCTGAGTGAATCTAGTAACTCGCGGA 1323
QY 1347 TCAGAATCCGCGGTGAATACGTTCCCGGCTTGTACACACCGCCCTCAACCATGGG 1406
Db 1324 TCAGAATCTCGCGGTGAATACGTTCCCGGCTTGTACACACCGCCCTCAACCATGGG 1383
QY 1407 AGTTGATTGCACAGAAAGTGTAGCTAA-CTTAGTGGGCGGATCACCAGGTGTGCT 1465
Db 1384 AGTGGTTGCAACAGAAAGTGTAGCTAAGTTCGGGAGGAGGTTACCGGTTGTAT 1443
QY 1466 CGATGACTGGGTTGAAGTCTGAAGTAGCCGTAGGGGAACCTCGGCTGGAATCAC 1523
Db 1444 TCATGACTGGGTTGAAGTCTGACCAAGTAGCCGTAGGGGAACCTCGGCTGGAATCAC 1501
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RESULT 8
US-10-218-519-5
; Sequence 5, Application US/10218519
; Publication No. US20030049806A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Takeshi
; APPLICANT: Imamura, Takeshi
; APPLICANT: Suda, Sakae
; APPLICANT: Honma, Tsutomu
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthesis and Gene Encoding the Same Enzy
; FILE REFERENCE: 03500.015225.1
; CURRENT APPLICATION NUMBER: US/10/219,519
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/821,016
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii Pl61 ; BP-7376
; FEATURE: cdna to 16S rRNA
US-10-218-519-5

Query Match 72.08; Score 1098.6; DB 14; Length 1501;
Best Local Similarity 85.98; Pred. No. 2.3e-289;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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QY 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
Db 9 GCGCGCAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCTGAATCA 66
QY 90 GAGCNGCCGAGCGGCTGAGTAATACTATTAGGAATCTAAGTAGTGGGGGATAGCTCGGG 149
Db 67 G---CGGCGGAGCGGTGAGTAATGCTTAGGAATCTGCTGTTAGTGGGGGCAACGCTCTC 123
QY 150 GAACTCGAATTAATACCCATACGT-CTACGGGAGAAACGAGCGGNTCAATAGACCTTG 208
Db 124 GAAAGGACGCTAATACCCATACGTCTACGGGAGAAACGAGGAGCTTCGGGCGCTTG 183
QY 209 CGCTATTAGATGAGCCTAAGTCGGAATAGCTAGATGCTGGGTAAGAGCCTACCATGGG 268
Db 184 CGCTATCAGATGAGCCTAGCTCGGATTAGCTAGTGGTGAATAGGCTACCAAGGCG 243
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QY	269	ACGATCTGAGCTGCTCTGAGAGGATGATACGCCACACCGGGAATGAGACACGGCCCGGA	328
Db	244	ACGATCCGTAAGTGTCTGAGAGGATGATCAGTCACTGGAACTGAGACACGGTCCAGA	303
QY	329	CT-CTACGGGAGCAGCAGTGGGGAATATTGGACAAATGNGGGAACCCCTGATCCAGCCAT	387
Db	304	CTCCTACGGAGGCACAGTGGGGAATATTGGACAAATGGCGAAAGCCTGATCCAGCCAT	363
QY	388	GCOCGTGTGTGAAGAAGGCOCTTTGTGTAAAGCACTTTTAAGCAGTGAAGAAGCACTCT	447
Db	364	GCOCGTGTGTGAAGAAGGCTTTCGGATTTGTAAGCACTTTTAAGTTGGGAGGAAGGCAT	423
QY	448	TCGGTTAATACCCGGGACGATGACATTAGCTGCAAGATTAAGCACACCGGCTACTCTGTGC	507
Db	424	TAACTTAATACGTTAGTGTTTTGACGTTACCGACAGAATTAAGCACCGGCTACTCTGTGC	483
QY	508	CAGCAGCCGCGGTAAATACAGAGGGTCAAGCGGTTAATCGGAATTACTTGGCGGTAAAGCA	567
Db	484	CAGCAGCCGCGGTAAATACAGAGGGTCAAGCGGTTAATCGGAATTACTTGGCGGTAAAGCGC	543
QY	568	CGGTAGTGGCTTGATTAAGTCAGATGTGAATAATCCCGGGCTTAACCTTGGGAACATCATCT	627
Db	544	CGGTAGTGGCTTGATTAAGTTGGATTTGAAGACCCCGGGCTCAACCTTGGGAACATCATCT	603
QY	628	GAAACTCTTAGCTAGACTAGTTCAGAGGGGAAAGTGAATTTTCAGTGTACGGGTGAATG	687
Db	604	AAAACTGACAACTAGATATGTTAGAGGTTGTTGGAATTTCTTGTTAGCGGTGAATG	663
QY	688	CGTAGAGTCTGAAGGAATACCGATGGCAAGGACAGCTTCTTGCAATCATATGACACTG	747
Db	664	CGTAGATATAGGAAGGAACACCACTGTCGCAAGCGCAACCACTTGGACTGATACTGACACTG	723
QY	748	AGGCTCGAAGAAGCGTGGGTAGCAACACAGGATTAAGTAFACCTTGTAGTCCAGCGGTAAAGC	807
Db	724	AGSTGCGAAGAGCGTGGGAGCAACACAGGATTAAGTACCTTGTAGTCCAGCGGTAAAGC	783
QY	808	ATGTCATAGTACGTTGGTGCCTTGTAGGACTTATGTAGCAGCAGCTAACGCAATTAAGTGA	867
Db	784	ATGTCAACTAGCGTTGGAGACCTTGTAGCTCTTGTAGCGGACGCTAACGCAATTAAGTGA	843
QY	868	CCGCTGGGGAGTAGCGGCCCAAGGTTAAACTCAAATGAATGACGGGGCCCGCACAA	927
Db	844	CCGCTGGGGAGTAGCGGCCCAAGGTTAAACTCAAATGAATGACGGGGCCCGCACAA	903
QY	928	CGGTGAGCATGTGGTTTAATTCGATGCAACCGCAAGCACTTACCTTGTCTTGACATA	987
Db	904	CGGTGAGCATGTGGTTTAATTCGAGCAACGCAAGCACTTACCGAGGCTTGCACATC	963
QY	988	CACAGAATCTTGTAGAGATACGAGTGCCTTCGGGAATTTGTATACAGTGTCTGATGG	1047
Db	964	CAATGAACTTTCAGAGATGATGGTGCCTTCGGGAATTTGACACAGTGTCTGATGG	1023
QY	1048	CTGTCGTAAGTCTGTCTGATGATGTTGGTTTAAGTCCCGCAACGAGCGCAACCTTGT	1107
Db	1024	CTGTCGTAAGTCTGTCTGATGATGTTGGTTTAAGTCCCGTAACGAGCGCAACCTTGT	1083
QY	1108	CCTTAGTTACCAGCAC- TTCGGTGGGAACTCTAGGATACTGCCAGTGAACACTGGAG	1166
Db	1084	CCTTAGTTACCAGCACGTAATGTTGGCACTCTTAAGAGACTGCCGCTGACAAACCGGAC	1143
QY	1167	GAAGCGGGGAGAGCTCAAGTCAATCATGTCGCCCTTACGACCGGGCTTACACAGTGTAC	1226
Db	1144	GAAGTGGGATGACGTCAGTCAATCATGTCGCCCTTACGCGCTTGGCTTACACAGTGTAC	1203
QY	1227	AATGGTAGTACAGAGGGCACTACACAGCGATGTGATGCGAATCTCAAAAACGCTATCG	1286
Db	1204	AATGGTCGTACAGAGGGTTCGCAAGCGCGAGGTGGAGCTAATCCACAAAACGATCG	1263
QY	1287	TAGTCCAGATTGGAGTCTGCAACTCGACTCCATCAATGAAGTACGAATCGTAGTAATCGCGGA	1346
Db	1264	TAGTCCGGAATGCGAGTCTGCAACTCGACTCGGTGAAGTCCGAATCGTAGTAATCGGAA	1323

QY	1347	TCAGAANTCGCGGTGAATACGTTCCCGGGCCCTGTACACACCGCCCGTGCACACCATGGG	1406
Db	1324	TCAGAATGTCGGGTGAATAGTTCCCGGGCCCTGTACACACCGCCCGTGCACACCATGGG	1383
QY	1407	AGTTGATTGCACACAGAAGTGGTTAGCCCTAA-CTTAGTGAGGGCCGATCACCACGGTGTGGT	1465
Db	1384	AGTGGGTTGCACAGAAGTAGCTAGTCTAACCCTCGGGAGGACGGTTACCAAGGTGTGAT	1443
QY	1466	CGATGACTCGGGTGAAGTCGTAAACAAGGTAGCCGTAGGGGAACCTGCGGGCTGGATCAC	1523
Db	1444	TCATGACTGGGGTGAAGTCGTACCAAGTAGCCGTAGGGGAACCTGCGGGCTGGATCAC	1501

RESULT 9

US-10-266-787-5

; Sequence 5, Application US/10266787

; Publication No. US20030082777A1

; GENERAL INFORMATION:

; APPLICANT: Yano, Tetsuya

; APPLICANT: Imamura, Takeshi

; APPLICANT: Suda, Sakae

; APPLICANT: Honma, Tsutomu

; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzym

; FILE REFERENCE: 03500.015225.3

; CURRENT APPLICATION NUMBER: US/10/266.787

; CURRENT FILING DATE: 2002-10-09

; PRIOR APPLICATION NUMBER: JP 2000-095004

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: Microsoft Word

; SEQ ID NO 5

; LENGTH: 1501

; TYPE: DNA

; ORGANISM: Pseudomonas jessenii P161 ; BP-7376

; FEATURE:

; FEATURE: cDNA to 16S rRNA

US-10-266-787-5

Query Match 72.0%; Score 1098.6; DB 14; Length 1501;


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Db 964 CAATGAATTTCCAGAGATGGATGGGTGCTTCGGGAACATTTAGACAGGTGCTGCATGG 1023
QY 1048 CTGTCTCAGCTCGTGTCTGTGAGATGTTGGGTTAACTCCCGCAACAGCGCAACCCCTTGT 1107
Db 1024 CTGTCTCAGCTCGTGTCTGTGAGATGTTGGGTTAACTCCCGCAACAGCGCAACCCCTTGT 1083
QY 1108 CATTAGTTTACCAGCAC--TTCCGGTGGGAACCTCTAAGGATATCTGCCAGTGCACAAACTGGAG 1166
Db 1084 CATTAGTTTACCAGCACGTAATGGTGGGCACCTCTAAGGATATCTGCCAGTGCACAAACTGGAG 1143
QY 1167 GAAGCGGGGAGCAGCFCRAAGTCAATATGGCCCTTACGACACAGGGGTACACACGCTGTAC 1226
Db 1144 GAAGTGGGGATGAGCTCAAGTCAATCATGGCCCTTACGGCTGGGTACACACGCTGTAC 1203
QY 1227 AATGTAGTACAGGCGCAGCTACACAGCGATGTGATCGGAATCTCAAAAAGCCTATCG 1286
Db 1204 AATGTCTGGTACAGAGGGTTGCCAAGCGCGAGGTGGAGTAACTCCCAANAACCGATCG 1263
QY 1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATCAAGTGAAGTCTAGTAACTCCCGGA 1346
Db 1264 TAGTCCGATCGCACTGCAACTCGACTCGGTGAAGTCTAGTAACTCCCGGA 1323
QY 1347 TCAGAAATCCCGGCTGAATACGTTCCCGGGCCCTTGTACACACCGCCCTGCACACATGGG 1406
Db 1324 TCAGAAATCCCGGCTGAATACGTTCCCGGGCCCTTGTACACACCGCCCTGCACACATGGG 1383
QY 1407 AGTTGATGACACAGAGTGGTGTAGCTTAA--CTTAGTACGGGGATCACACGCTGTGGT 1465
Db 1384 AGTGGGTTGCACCAAGATGAGTCTTAACCTTCGGGAGACGGTTACCGGGTGTGAT 1443
QY 1466 CGATGACTGGGCTGAAGTCTGAACAGTGTAGCCGTAGGGAACCTCGGCTGGATCAC 1523
Db 1444 TCATGACTGGGCTGAAGTCTGAACAGTGTAGCCGTAGGGAACCTCGGCTGGATCAC 1501

RESULT 12
US-10-133-404A-1
; Sequence 1, Application US/10133404A
; Publication No. US20030104302A1
; GENERAL INFORMATION:
; APPLICANT: Tsutomu Honma
; APPLICANT: Tetsuya Yano
; APPLICANT: Tsuyoshi No. US20030104302A1oto
; APPLICANT: Shinya Kozaki
; TITLE OF INVENTION: Construct and Method for Making It
; FILE REFERENCE: CF016374
; CURRENT APPLICATION NUMBER: US/10/133,404A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: JP P2001-131694
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP P2001-208704
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
US-10-133-404A-1

Query Match 72.0%; Score 1098.6; DB 14; Length 1501;
Best Local Similarity 85.9%; Pred. No. 2.3e-289;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GGGGCGAGCTTACACATCAAGTCTGAGCGGAACAGATGATAGCTTGTCTATAGGCTC 89
Db 9 GGGGCGAGCTTACACATCAAGTCTGAGCGG--ATGACGGGAGCTTGTCTCTGAATCA 66
QY 90 GAGCGCGGAGCGGTGAGTAACTTACCTAGGAATCTTACCTAGTCTAGTGGGGATCTCGG 149
Db 67 G---CGGCGGAGCGGTGAGTAACTGCTAGGAATCTTGTCTGAGTGGGGAGACAGCTC 123
QY 150 GAACTCGAATTAATACCGATACGT--CTACGGGAGAAAGCAGGGNCTATTAGACCTTG 208
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Db 124 GAAAGGAGCGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCGCTTG 183
QY 209 CGCTATTAGATGACCCCTAAGTCCGATTCGATAGATGGTGGGCTAAAGGCGCTACCATGGCG 268
|||||
Db 184 CGCTATCAGATGACCCCTAGTCCGATTCGATAGTGGTGGTAAAGTGGCTACCAAGCGC 243
QY 269 AGATCTCTAGCTGTCTGAGAGGATGATACCCACACCGGAGTGGAGACACGGCCCGCA 328
|||||
Db 244 AGATCCGCTAAGTCTGAGAGGATGATCAGTCACTGGAATGAGACACGGTCCAG 303
QY 329 CT--CTACGGGAGCAGCAGTGGGAAATATTGGACAATGGNGGAAACCCCTGATCCAGCCAT 387
|||||
Db 304 CTCCTACGGGAGCAGCAGTGGGAAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363
QY 388 GCGCGCTGTCTCAAGAGGCGCTTTTGGTTGTAAGCACCTTTAAGCAGTGAAGAACTCT 447
|||||
Db 364 GCGCGCTGTGTGAAGAGGCTTTCGGATTGTAAGCACCTTTAAGTTGGAGGAAGGCGAT 423
QY 448 TCGGTTAATACCGGGGACCATGACATTAGCTGCAGAATAAGACACCGGCTTAACCTCTGTGC 507
|||||
Db 424 TAACTAATACGTTAGTGTGTTGACGTTACGACAGATAGACACCGGCTAAGTCTGTGC 483
QY 508 CAGCAGCGCGGTAAATACAGAGGTCGAAGCGTTAATCGGAATTTACTGGGCGTAAAGCGA 567
|||||
Db 484 CAGCAGCGCGTAAATACAGAGGTCGAAGCGTTAATCGGAATTTACTGGGCGTAAAGCGC 543
QY 568 GCGTAGTGGCTTGTATAGTACAGATCTGAATCCCGGGCTTACCTGGGAGTGCATCT 627
|||||
Db 544 GCGTAGTGGCTTGTATAGTGGATGTGAAGCCCCGGGCTCAACCTTGGGAACTGATCTC 603
QY 628 GAAACTGTTAGCTAGATAGTGGTGAAGGGAAGTGAATTTTACGAGTGTAGCGTGAATATG 687
|||||
Db 604 AATAGCTCAAGCTAGAGTATGGTGAAGGTTGGTGAATTTTCTGTCTAGCGTGAATG 663
QY 688 CGTAGAGTCTGAAGGAATACCGATCGGAGAGCGACTTCTCGCATCAPACTGACATCTG 747
|||||
Db 664 CTTAGATATAGGAAGAACCCAGTGGGAGCGGACCCCTTGGACTGATACCTGACATCT 723
QY 748 AGGCTCGAAGCGTGGGTAGCAACAGGATAGATACCTGCTAGTCCACGCGGTAAAGC 807
|||||
Db 724 AGGTGGAAGCGTGGGAGCAACAGGATAGTACCTCTGTAGTCCAGCGCGTAAAGC 783
QY 808 ATGCTTACTAGTCTGGTCCCTTGAGGACTTAGTGACGAGCTAAGCAACGAAATAGTAGA 867
|||||
Db 784 ATGCTAATAGCCGTTGGAGCCCTTGAAGTCTTATGCGGAGCTAAGCAATTAAGTTGA 843
QY 868 CGGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATGACGGGGGCGCCGACAA 927
Db 844 CGGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATGACGGGGGCGCCGACAA 903
QY 928 GCGGTGGAGCATGTGGTTAATTCGATGCAACGCAAGAACCTTACCTGCTCTTGACATA 987
Db 904 GCGGTGGAGCATGTGGTTAATTCGAGACACGCAAGAACCTTACCGGCTTGAATCTC 963
QY 988 CACAGAATCTTGTAGATACGAGTGGCTTCGGGAAATTTGTGATACAGGTGCTGATCG 1047
|||||
Db 964 CAATGAATTTCCAGAGATGGATGGGTCCTTCGGGAACATTTAGACAGTGTGCTGATCG 1023
QY 1048 CTGTCTCAGCTCGTGTCTGTGAGATGTTGGGTTAACTCCCGCAACAGCGCAACCCCTTGT 1107
Db 1024 CTGTCTCAGCTCGTGTCTGTGAGATGTTGGGTTAACTCCCGCAACAGCGCAACCCCTTGT 1083
QY 1108 CATTAGTTTACCAGCAC--TTCCGGTGGGAACCTCTAAGGATATCTGCCAGTGCACAAACTGGAG 1166
Db 1084 CATTAGTTTACCAGCACGTAATGGTGGGCACCTCTAAGGATATCTGCCAGTGCACAAACTGGAG 1143
QY 1167 GAAGCGGGGAGCAGCTCAAGTCAATCATGCCCTTACGACACAGGGGTACACAGCTGTAC 1226
Db 1144 GAAGTGGGGATGAGCTCAAGTCAATCATGGCCCTTACGGCTGGGTACACACGCTGTAC 1203
QY 1227 AATGTAGTACAGGCGCAGCTACACAGCGATGTGATCGGAATCTCAAAAAGCCTATCG 1286
Db 1204 AATGTCTGGTACAGAGGGTTGCCAAGCGCGAGGTGGAGTAACTCCCAANAACCGATCG 1263
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QY 1287 TACTCCAGATTGGAGTCTGCAACTCGACTCCATGAGTAACTAGTAACTGCGGA 1346
DB 1264 TAGTCCGGATTCAGTCTGCAACTCGAGTCCGTTGAGTGGGAATCGTAGTATCGGAA 1323
QY 1347 TCAGAAATGCGCGGTGAATAGCTTCCCGGGCTTGTACACACCGCGCTCACACCATGGG 1406
DB 1324 TCAGAAATGCGCGGTGAATAGCTTCCCGGGCTTGTACACACCGCGCTCACACCATGGG 1383
QY 1407 AGTTGATTCCACAGAAAGTGTAGTAACTTCTAGTGGGGGATCACACCGTGTGGT 1465
DB 1384 AGTGGGTTCCACAGAAAGTGTAGTAACTTCTAGTGGGGGATCACACCGTGTGGT 1443
QY 1466 CGATGACTGGGTGAAGTGAATGCAAGTGAAGTGGGAACTCGGGTGGATCAC 1523
DB 1444 TCATGACTGGGTGAAGTGAATGCAAGTGAAGTGGGAACTCGGGTGGATCAC 1501

RESULT 13
US-10-007-725-5
; Sequence 5, Application US/10007725
; Publication No. US20020150887A1
; GENERAL INFORMATION:
; APPLICANT: Maruyama, Akihiko
; APPLICANT: Higashihara, Takanori
; APPLICANT: Kitamura, Keiko
; APPLICANT: Sunamura, Michinari
; APPLICANT: Kurane, Ryuichiro
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID PROBES FOR
; TITLE OF INVENTION: MOLECULAR GENETIC ANALYSIS OF POLLUTED ENVIRONMENTS AND
; FILE OF INVENTION: ENVIRONMENTAL SAMPLES
; FILE REFERENCE: 13558-003001
; CURRENT APPLICATION NUMBER: US/10/007,725
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: JP 341765/2000
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: GR211-P1(FERM P-17394)
US-10-007-725-5

Query Match 71.5%; Score 1090.4; DB 13; Length 1494;
Best Local Similarity 86.4%; Pred. No. 4e-287;
Matches 1271; Conservative 0; Mismatches 194; Indels 6; Gaps 6;

QY 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAGATGATGCTTCTATAGCGGTC 89
DB 25 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAGATGCTTCTATAGCGGTC 84
QY 90 GAGCNGCCGACGGGTGAGTAACTTAGGAATCTACCTAGTGGGGATGCTCGGG 149
DB 85 GAGCGG-CGGACGGGTGAGTAACTTAGGAATCTACCTAGTGGGGATGCTCGGG 143
QY 150 GAAACTCGAATTAATACCGCAT-ACGCTACGGGAGAAAAGCAGGGGNTCAATAGACCTTG 208
DB 144 GAAACCCAGCATTAATACCGCATATCCCTACGGGGGAAAGCAGGGGATCTTCGGACCTTG 203
QY 209 CGCTATTAGATGAGCTTAATGCGGATGATGATGATGATGATGATGATGATGATGATG 268
DB 204 TCCTGATGGATGAGTTCGCGTTCGATGATGATGATGATGATGATGATGATGATGATG 263
QY 269 ACGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 328
DB 264 ACGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 323
QY 329 CT-CTACGGGAGCAGTGGGGAATATTGGCAATGGGGAACCTGATCCAGCCAT 387
DB 324 CTCCTACGGGAGCAGTGGGGAATATTGGCAATGGGGAACCTGATCCAGCCAT 383

QY 388 GCGCGCTGTGCAAGAGCGCTTTTGGTTGTAAGCACTTTAAGCAGTGAAGAGACTCT 447
DB 384 GCGCGCTGTGTGAAGAGAGCGCTTCGGGTTGTAAGAGCACTTTAAGTGAAGAGAGGCTTA 443
QY 448 TCGGTTAATACCCCGGGAGCAGTACATAGCTGCAGAAATAAGCACACCGCGCTTAACCTGTGTC 507
DB 444 TCCTTAATACCGATGAGTACTTGAAGTACCTACAGAGAGCAGCGCTTAATTTCTGTCG 503
QY 508 CACACCGCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAATTAATCGGCTGAAGCGA 567
DB 504 CAGCAGCGCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAATTAATCGGCTGAAGCGC 563
QY 568 GCGTGTGCTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 627
DB 564 GCGTGTGCTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 623
QY 628 GAAACTGTTAGCTAGTGTAGAGAGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 687
DB 624 GAAACTGCGAGCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 683
QY 688 CGTAGAGATCTGAAGAGTACCGATGCGAGAGCAGCTTCCGTGCATCATCATCATCATCAT 747
DB 684 CGTAGAGATCTGAAGAGTACCGATGCGAGAGCAGCTTCCGTGCATCATCATCATCATCAT 743
QY 748 AGGCTCGAAAGCGTGGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 807
DB 744 AGGCTCGAAAGCGTGGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 803
QY 808 ATGTCTACTAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 866
DB 804 ATGTCTACTAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 863
QY 867 ACCGCTGGGGAGTACGCGCGCAAGGTTAACTCAATGAATGAATGAATGAATGAATGAATGA 926
DB 864 ACCGCTGGGGAGTACGCGCGCAAGGTTAACTCAATGAATGAATGAATGAATGAATGAATGA 923
QY 927 AGCGGTGGAGCATGTGGTTAATTCGATGCAAGCGCAAGAACCTTACCTGGTCTTGACAT 986
DB 924 AGCGGTGGAGCATGTGGTTAATTCGATGCAAGCGCAAGAACCTTACCTGGTCTTGACAT 983
QY 987 ACACAGAACTTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1046
DB 984 CCTTGAAGTCTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1043
QY 1047 GCTGTGCTGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1106
DB 1044 GCTGTGCTGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1103
QY 1107 TCCTTAGTTACAGCAC-TTCGGGTGGGAACTTAAGGATGATGATGATGATGATGATGATGATG 1165
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DB 1164 GGAAGTGGGGAGCAGCTCAAGTCAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
QY 1226 CAATGTGTAGTACAGAGGCGAGCTACACAGCTGATGATGATGATGATGATGATGATGATGATG 1285
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RESULT 15
US-09-726-774-3
; Sequence 3, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-726-774-3

Query Match 70.2%; Score 1070.8; DB 9; Length 1467;
Best Local Similarity 85.9%; Pred. No. 8.8e-282;
Matches 1233; Conservative 0; Mismatches 199; Indels 4; Gaps 4;

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Job time : 1528.06 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 00:33:30 ; Search time 71.3884 Seconds
(without alignments)
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Scoring table: IDENTITY_NOC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
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- 3: gb_in.*
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- 6: gb_pat.*
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- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
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- 20: em_om.*
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- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	19	100.0	19	6	E58428	E58428 DNA probe f
2	19	100.0	300	1	AF025555	AF025555 Psychroba
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4	19	100.0	1462	1	AB094458	AB094458 Psychroba
5	19	100.0	1520	1	AB016059	AB016059 Psychroba
6	19	100.0	1525	1	AB016056	AB016056 Psychroba
7	19	100.0	1526	1	AB016057	AB016057 Psychroba
8	19	100.0	1526	6	E58427	E58427 DNA probe f
9	19	100.0	1530	1	AB016058	AB016058 Psychroba
10	19	100.0	1531	1	AB016055	AB016055 Psychroba
11	19	100.0	1536	1	AB016054	AB016054 Psychroba
12	17.4	91.6	161	1	AF440839	AF440839 Unculture
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14	17.4	91.6	168	1	AF440851	AF440851 Unculture
15	17.4	91.6	170	1	AF440834	AF440834 Unculture
16	17.4	91.6	170	1	AF440837	AF440837 Unculture
17	17.4	91.6	171	1	AF440838	AF440838 Unculture
18	17.4	91.6	172	1	AF128774	AF128774 Unculture
19	17.4	91.6	172	1	AF440831	AF440831 Unculture
20	17.4	91.6	174	1	AF440842	AF440842 Unculture
21	17.4	91.6	175	1	AF440832	AF440832 Unculture
22	17.4	91.6	175	1	AF440846	AF440846 Unculture
23	17.4	91.6	177	1	AF128777	AF128777 Unculture
24	17.4	91.6	691	1	AY159801	AY159801 Psychroba
25	17.4	91.6	692	1	AY159792	AY159792 Psychroba
26	17.4	91.6	700	1	PSP244767	PSP244767 Psychroba
27	17.4	91.6	717	1	PSP244768	PSP244768 Psychroba
28	17.4	91.6	880	1	AF513419	AF513419 Psychroba
29	17.4	91.6	1354	1	AF505742	AF505742 Bacterium
30	17.4	91.6	1401	1	AF505736	AF505736 Bacterium
31	17.4	91.6	1409	1	PSU85874	PSU85874 Psychrobact
32	17.4	91.6	1425	1	AF505724	AF505724 Gamma pro
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34	17.4	91.6	1426	1	PSP272303	PSP272303 Psychroba
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37	17.4	91.6	1445	1	AF468383	AF468383 Arctic se
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45	17.4	91.6	1462	1	PGU85877	PGU85877 Psychrobact

ALIGNMENTS

RESULT 1
E58428
LOCUS E58428
DEFINITION DNA probe for detecting novel psychrophile.
ACCESSION E58428
VERSION E58428.1 GI:18622290
KEYWORDS JP 2000333680-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Maruyama,A., Kitamura,K. and Kurane,R.
TITLE DNA probe for detecting novel psychrophile
JOURNAL Patent: JP 2000333680-A 2 05-DEC-2000;
AGENCY OF IND SCIENCE & TECHNOL

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COMMENT      OS      Artificial Sequence
PN      JP      2000333680-A/2
PD      05-DEC-2000
PF      25-MAY-1999      JP      1999145342
PR
PI      AKIHIKO MARYAMA, KEIKO KITAMURA, RYUICHIRO KURANE
C12N15/09, C12N1/20, C12G1/68//C12N15/09, C12R1/01, (C12N1/20, PC
C12R1/01),
PC      C12N15/00, (C12N15/00, C12R1/01)
CC
FH      Key      Location/Qualifiers
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FT      Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 40;
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DEFINITION      Psychrobacter glacincola 16S ribosomal RNA gene, partial sequence.
ACCESSION      AF025555
VERSION      AF025555.1 GI:2582456
KEYWORDS
SOURCE      Psychrobacter glacincola
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE      1 (bases 1 to 300)
            Hagstrom, A., Pinhassi, J. and Zweifel, U.L.
            Biogeographical diversity among marine bacterioplankton
            Aquat. Microb. Ecol. 21, 231-244 (2000)
JOURNAL
AUTHORS      Pinhassi, J., Zweifel, U.L. and Hagstrom, A.
TITLE      Direct Submission
SUBMITTED (18-SEP-1997) National Environmental Research Institute,
Frederiksborgvej 399, Roskilde DK-4000, Denmark
LOCATION/Qualifiers
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LOCUS      Psychrobacter sp. MJYP.15.12 gene for 16S rRNA, partial sequence.
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ACCESSION      AB094456
VERSION      AB094456.1 GI:27807566
KEYWORDS
ORGANISM      Psychrobacter sp. MJYP.15.12
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE      1
            Inagaki, F., Suzuki, M., Takai, K. and Horikoshi, K.
            Microbial community structure in subseafloor sediments from the Sea
            of Okhotsk
            Published Only in Database (2003)
JOURNAL
AUTHORS      Inagaki, F.
TITLE      Direct Submission
SUBMITTED (23-OCT-2002) Fumio Inagaki, Japan Marine Science &
Technology Center, Subground Animalcule Retrieval (SUGAR) Project,
Frontier Research System for Extremophiles; Natsuchina-cho 2-15,
Yokosuka 237-0061, Japan (E-mail: inagaki@jamstec.go.jp,
Tel: 81-468-67-9687, Fax: 81-468-67-9715)
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 39;
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RESULT 4
AB094458/c
LOCUS      Psychrobacter sp. MJYP.25.32 gene for 16S rRNA, partial sequence.
DEFINITION      Psychrobacter sp. MJYP.25.32
ACCESSION      AB094458
VERSION      AB094458.1 GI:27807568
KEYWORDS
ORGANISM      Psychrobacter sp. MJYP.25.32
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE      1
            Inagaki, F., Suzuki, M., Takai, K. and Horikoshi, K.
            Microbial community structure in subseafloor sediments from the Sea
            of Okhotsk
            Published Only in Database (2003)
JOURNAL
AUTHORS      Inagaki, F.
TITLE      Direct Submission
SUBMITTED (23-OCT-2002) Fumio Inagaki, Japan Marine Science &
Technology Center, Subground Animalcule Retrieval (SUGAR) Project,
Frontier Research System for Extremophiles; Natsuchina-cho 2-15,
Yokosuka 237-0061, Japan (E-mail: inagaki@jamstec.go.jp,
Tel: 81-468-67-9687, Fax: 81-468-67-9715)
LOCATION/Qualifiers
FEATURES
source      1. .1462
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
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Db 456 TAATGTCATCGTCCCGGG 438

RESULT 5
AB016059/c
LOCUS
DEFINITION
Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain: NIBH P2K18.
AB016059
ACCESSION
AB016059 1 GI:6691640
VERSION
16S ribosomal RNA.
KEYWORDS
Psychrobacter pacificensis
SOURCE
Psychrobacter pacificensis
Organism
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE
1 (sites)
Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
Phylogenetic analysis of psychrophilic bacteria isolated from the
Japan Trench, including a description of the deep-sea species
Psychrobacter pacificensis sp. nov
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
JOURNAL
MEDLINE
20222194
PUBMED
10758895
REFERENCE
2 (bases 1 to 1520)
Maruyama,A. and Kitamura,K.
Direct Submission
TITLE
Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
Bioscience and Human-Technology, Department of Applied and
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,
Fax:+81-298-54-6412)
FEATURES
Location/Qualifiers
1..1520
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BASE COUNT 398 a 334 c 468 g 325 t
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Query Match 100.0%; Score 19; DB 1; Length 1525;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
|||||
Db 473 TAATGTCATCGTCCCGGG 455

RESULT 7
AB016057/c
LOCUS
DEFINITION
Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain: NIBH P2K6(T)(=IFO 16279(T)).
AB016057
ACCESSION
AB016057 1 GI:6691638
VERSION
16S ribosomal RNA.
KEYWORDS
Psychrobacter pacificensis
SOURCE
Psychrobacter pacificensis
Organism
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE
1 (sites)
Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
Phylogenetic analysis of psychrophilic bacteria isolated from the
Japan Trench, including a description of the deep-sea species
Psychrobacter pacificensis sp. nov
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
JOURNAL
MEDLINE
20222194
PUBMED
10758895
REFERENCE
2 (bases 1 to 1526)
Maruyama,A. and Kitamura,K.
Direct Submission
TITLE
Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
Bioscience and Human-Technology, Department of Applied and
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,
Fax:+81-298-54-6412)
FEATURES
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1..1526
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/db_xref="taxon:112002"
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/product="16S ribosomal RNA"
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
|||||
Db 472 TAATGTCATCGTCCCGGG 454

RESULT 6
AB016056/c
LOCUS
DEFINITION
Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain: NIBH P2J13.
AB016056
ACCESSION
AB016056 1 GI:6691637
VERSION
16S ribosomal RNA.
KEYWORDS
Psychrobacter pacificensis
SOURCE
Psychrobacter pacificensis
Organism
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE
1 (sites)
Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
Phylogenetic analysis of psychrophilic bacteria isolated from the
Japan Trench, including a description of the deep-sea species
Psychrobacter pacificensis sp. nov
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
JOURNAL
MEDLINE
20222194
PUBMED
10758895
REFERENCE
2 (bases 1 to 1526)
Maruyama,A. and Kitamura,K.
Direct Submission
TITLE
Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
Bioscience and Human-Technology, Department of Applied and
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,
Fax:+81-298-54-6412)
FEATURES
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BASE COUNT 398 a 332 c 467 g 322 t 1 others
ORIGIN

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
|||||
Db 472 TAATGTCATCGTCCCGGG 454

RESULT 6
AB016056/c
LOCUS
DEFINITION
Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain: NIBH P2J13.
AB016056
ACCESSION
AB016056 1 GI:6691637
VERSION
16S ribosomal RNA.
KEYWORDS
Psychrobacter pacificensis
SOURCE
Psychrobacter pacificensis
Organism
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE
1 (sites)
Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
Phylogenetic analysis of psychrophilic bacteria isolated from the
Japan Trench, including a description of the deep-sea species
Psychrobacter pacificensis sp. nov
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
JOURNAL
MEDLINE
20222194
PUBMED
10758895
REFERENCE
2 (bases 1 to 1526)
Maruyama,A. and Kitamura,K.
Direct Submission
TITLE
Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
Bioscience and Human-Technology, Department of Applied and
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,
Fax:+81-298-54-6412)
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
|||||
Db 472 TAATGTCATCGTCCCGGG 454

RESULT 6
AB016056/c
LOCUS
DEFINITION
Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain: NIBH P2J13.
AB016056
ACCESSION
AB016056 1 GI:6691637
VERSION
16S ribosomal RNA.
KEYWORDS
Psychrobacter pacificensis
SOURCE
Psychrobacter pacificensis
Organism
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE
1 (sites)
Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
Phylogenetic analysis of psychrophilic bacteria isolated from the
Japan Trench, including a description of the deep-sea species
Psychrobacter pacificensis sp. nov
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
JOURNAL
MEDLINE
20222194
PUBMED
10758895
REFERENCE
2 (bases 1 to 1526)
Maruyama,A. and Kitamura,K.
Direct Submission
TITLE
Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
Bioscience and Human-Technology, Department of Applied and
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,
Fax:+81-298-54-6412)
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BASE COUNT 398 a 332 c 467 g 322 t 1 others
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Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
|||||
Db 472 TAATGTCATCGTCCCGGG 454

RESULT 6
AB016056/c
LOCUS
DEFINITION
Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain: NIBH P2J13.
AB016056
ACCESSION
AB016056 1 GI:6691637
VERSION
16S ribosomal RNA.
KEYWORDS
Psychrobacter pacificensis
SOURCE
Psychrobacter pacificensis
Organism
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE
1 (sites)
Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
Phylogenetic analysis of psychrophilic bacteria isolated from the
Japan Trench, including a description of the deep-sea species
Psychrobacter pacificensis sp. nov
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
JOURNAL
MEDLINE
20222194
PUBMED
10758895
REFERENCE
2 (bases 1 to 1526)
Maruyama,A. and Kitamura,K.
Direct Submission
TITLE
Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
Bioscience and Human-Technology, Department of Applied and
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,
Fax:+81-298-54-6412)
FEATURES
Location/Qualifiers
1..1526
/organism="Psychrobacter pacificensis"
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/strain="NIBH P2K6(T)(=IFO 16279(T))"
/db_xref="taxon:112002"
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/product="16S ribosomal RNA"
BASE COUNT 398 a 332 c 467 g 322 t 1 others
ORIGIN

Query Match 100.0%; Score 19; DB 1; Length 1520;

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BASE COUNT 401 a 332 c 467 g 323 t 3 others

ORIGIN

Query Match 100.0%; Score 19; DB 1; Length 1526;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19

Db 476 TAATGTCATCGTCCCGGG 458

RESULT 8
E58427/c
LOCUS E58427 1526 bp DNA linear PAT 31-JAN-2002
DEFINITION DNA probe for detecting novel psychrophile.
ACCESSION E58427

VERSION E58427.1 GI:18622289
KEYWORDS JP 2000333680-A/1.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1526)
AUTHORS Maruyama,A., Kitamura,K. and Kurane,R.
TITLE DNA probe for detecting novel psychrophile
JOURNAL Patent: JP 2000333680-A 1 05-DEC-2000;
AGENCY OF IND SCIENCE & TECHNOL

COMMENT OS Psychrobacter pacificus
PN JP 2000333680-A/1
PD 05-DEC-2000
PF 25-MAY-1999 JP 1999145342

PR PI AKIHIKO MARYAMA,KEIKO KITAMURA,RYUICHIRO KURANE PC
C12N15/09,C12N1/20,C12Q1/68//C12N15/09,C12R1:01),(C12N1/20, PC
C12R1:01),
PC C12N15/00,(C12N15/00,C12R1:01)
CC

FT Key Key Location/Qualifiers
rRNA (1)..(1526).

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BASE COUNT 401 a 332 c 467 g 323 t 3 others

ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 1526;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19

Db 476 TAATGTCATCGTCCCGGG 458

RESULT 9
AB016058/c
LOCUS AB016058 1530 bp DNA linear BCT 10-MAY-2000
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain:NIH P2J3.

ACCESSION AB016058
VERSION AB016058.1 GI:6691639

KEYWORDS 16S ribosomal RNA
SOURCE Psychrobacter pacificensis
ORGANISM Psychrobacter pacificensis

REFERENCE 1 (sites)
AUTHORS Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the
Japan Trench, including a description of the deep-sea species

Psychrobacter pacificensis sp. nov
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
20222194
PUBMED 10758895
REFERENCE 2 (bases 1 to 1530)
AUTHORS Maruyama,A. and Kitamura,K.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
Bioscience and Human-Technology, Department of Applied and
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
Japan (E-mail:maruyama@nih.go.jp, Tel:+81-298-54-6062,
Fax:+81-298-54-6412)

FEATURES
source
1..1530
/organism="Psychrobacter pacificensis"
/mol_type="genomic DNA"
/strain="NIH P2J3"
/db_xref="taxon:112002"
<1..>1530
/product="16S ribosomal RNA"

BASE COUNT 401 a 331 c 472 g 326 t

ORIGIN

Query Match 100.0%; Score 19; DB 1; Length 1530;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19

Db 478 TAATGTCATCGTCCCGGG 460

RESULT 10
AB016055/c

LOCUS AB016055 1531 bp DNA linear BCT 10-MAY-2000
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
strain:NIH P2J3.

ACCESSION AB016055
VERSION AB016055.1 GI:6691636

KEYWORDS 16S ribosomal RNA
SOURCE Psychrobacter pacificensis
ORGANISM Psychrobacter pacificensis

REFERENCE 1 (sites)
AUTHORS Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the
Japan Trench, including a description of the deep-sea species

Psychrobacter pacificensis sp. nov
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
20222194
PUBMED 10758895
REFERENCE 2 (bases 1 to 1531)
AUTHORS Maruyama,A. and Kitamura,K.
TITLE Direct Submission

JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
Bioscience and Human-Technology, Department of Applied and
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
Japan (E-mail:maruyama@nih.go.jp, Tel:+81-298-54-6062,
Fax:+81-298-54-6412)

FEATURES
source
1..1531
/organism="Psychrobacter pacificensis"
/mol_type="genomic DNA"
/strain="NIH P2J3"
/db_xref="taxon:112002"
<1..>1531
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BASE COUNT 400 a 332 c 470 g 324 t 5 others

ORIGIN

Query Match 100.0%; Score 19; DB 1; Length 1531;
Best Local Similarity 100.0%; Pred. No. 39;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAATGTCATCGTCCCGGG 19
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Db 484 TAATGTCATCGTCCCGGG 466

RESULT 11
AB016054/c
LOCUS      1536 bp      DNA      linear      BCT 10-MAY-2000
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
            strain.NIBH P2J2.
ACCESSION AB016054
VERSION   AB016054.1 GI:6691635
KEYWORDS  16S ribosomal RNA.
SOURCE    Psychrobacter pacificensis
ORGANISM  Psychrobacter pacificensis
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE 1 (sites)
AUTHORS   Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
TITLE     Phylogenetic analysis of psychrophilic bacteria isolated from the
            Japan Trench, including a description of the deep-sea species
            Psychrobacter pacificensis sp. nov
JOURNAL   Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
MEDLINE   20222194
PUBMED    10758895
REFERENCE 2 (bases 1 to 1536)
AUTHORS   Maruyama,A. and Kitamura,K.
TITLE     Direct Submission
JOURNAL   Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
            Bioscience and Human-Technology, Department of Applied and
            Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
            Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,
            Fax:+81-298-54-6412)
FEATURES   Location/Qualifiers
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            1..1536
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BASE COUNT 405 a 335 c 472 g 324 t
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Query Match 100.0%; Score 19; DB 1; Length 1536;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAATGTCATCGTCCCGGG 19
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Db 476 TAATGTCATCGTCCCGGG 458

RESULT 12
AF440839/c
LOCUS      161 bp      DNA      linear      BCT 25-NOV-2001
DEFINITION Uncultured gamma proteobacterium 16S ribosomal RNA gene, partial
            sequence.
ACCESSION AF440839
VERSION   AF440839.1 GI:17064094
KEYWORDS  uncultured gamma proteobacterium
SOURCE    uncultured gamma proteobacterium
ORGANISM  Bacteria; Proteobacteria; Gammaproteobacteria; environmental
            samples.
            1 (bases 1 to 161)
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Bioremediation Treatment Effects On Microbial Community Structure
            In A Crude Oil-Contaminated Coastal Marsh
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 161)

Qy 1 TAATGTCATCGTCCCGGG 19
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Db 476 TAATGTCATCGTCCCGGG 458

RESULT 13
AF440847/c
LOCUS      165 bp      DNA      linear      BCT 25-NOV-2001
DEFINITION Uncultured gamma proteobacterium DGGE band ns.st8.d3-II 16S
            ribosomal RNA gene, partial sequence.
ACCESSION AF440847
VERSION   AF440847.1 GI:17064102
KEYWORDS  uncultured gamma proteobacterium
SOURCE    uncultured gamma proteobacterium
ORGANISM  Bacteria; Proteobacteria; Gammaproteobacteria; environmental
            samples.
            1 (bases 1 to 165)
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Bioremediation Treatment Effects On Microbial Community Structure
            In A Crude Oil-Contaminated Coastal Marsh
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 165)
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Direct Submission
JOURNAL   Submitted (30-OCT-2001) Civil and Environmental Engineering,
            University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES   Location/Qualifiers
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            1..165
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                /db_xref="taxon:86473"
                /country="Canada: Nova Scotia"
                /note="oiled, nutrient-amended plots with existent plants
                    (phytoremediation treatment) in an oil bioremediation
                    field study conducted at a coastal marsh"
            <1..>165
                /product="16S ribosomal RNA"
BASE COUNT 47 a 34 c 50 g 34 t
ORIGIN
Query Match 91.6%; Score 17.4; DB 1; Length 165;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TAATGTCATCGTCCCGGG 19
    |||||
Db 147 TAATGTCATCGTCCCGGG 129

RESULT 14
AF440851/c
LOCUS      168 bp      DNA      linear      BCT 25-NOV-2001

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AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Direct Submission
JOURNAL   Submitted (30-OCT-2001) Civil and Environmental Engineering,
            University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES   Location/Qualifiers
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            1..161
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                /mol_type="genomic DNA"
                /db_xref="taxon:86473"
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            <1..>161
                /product="16S ribosomal RNA"
BASE COUNT 47 a 32 c 49 g 33 t
ORIGIN
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Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TAATGTCATCGTCCCGGG 19
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Db 147 TAATGTCATCGTCCCGGG 129

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RESULT 13
AF440847/c
LOCUS      165 bp      DNA      linear      BCT 25-NOV-2001
DEFINITION Uncultured gamma proteobacterium DGGE band ns.st8.d3-II 16S
            ribosomal RNA gene, partial sequence.
ACCESSION AF440847
VERSION   AF440847.1 GI:17064102
KEYWORDS  uncultured gamma proteobacterium
SOURCE    uncultured gamma proteobacterium
ORGANISM  Bacteria; Proteobacteria; Gammaproteobacteria; environmental
            samples.
            1 (bases 1 to 165)
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Bioremediation Treatment Effects On Microbial Community Structure
            In A Crude Oil-Contaminated Coastal Marsh
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 165)
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Direct Submission
JOURNAL   Submitted (30-OCT-2001) Civil and Environmental Engineering,
            University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES   Location/Qualifiers
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                /mol_type="genomic DNA"
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                    (phytoremediation treatment) in an oil bioremediation
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BASE COUNT 47 a 34 c 50 g 34 t
ORIGIN
Query Match 91.6%; Score 17.4; DB 1; Length 165;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TAATGTCATCGTCCCGGG 19
    |||||
Db 147 TAATGTCATCGTCCCGGG 129

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RESULT 13
AF440847/c
LOCUS      165 bp      DNA      linear      BCT 25-NOV-2001
DEFINITION Uncultured gamma proteobacterium DGGE band ns.st8.d3-II 16S
            ribosomal RNA gene, partial sequence.
ACCESSION AF440847
VERSION   AF440847.1 GI:17064102
KEYWORDS  uncultured gamma proteobacterium
SOURCE    uncultured gamma proteobacterium
ORGANISM  Bacteria; Proteobacteria; Gammaproteobacteria; environmental
            samples.
            1 (bases 1 to 165)
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Bioremediation Treatment Effects On Microbial Community Structure
            In A Crude Oil-Contaminated Coastal Marsh
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 165)
AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Direct Submission
JOURNAL   Submitted (30-OCT-2001) Civil and Environmental Engineering,
            University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES   Location/Qualifiers
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                    (phytoremediation treatment) in an oil bioremediation
                    field study conducted at a coastal marsh"
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BASE COUNT 47 a 34 c 50 g 34 t
ORIGIN
Query Match 91.6%; Score 17.4; DB 1; Length 165;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TAATGTCATCGTCCCGGG 19
    |||||
Db 147 TAATGTCATCGTCCCGGG 129

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```

RESULT 14
AF440851/c
LOCUS      168 bp      DNA      linear      BCT 25-NOV-2001

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```

Qy 1 TAATGTCATCGTCCCGGG 19
    |||||
Db 147 TAATGTCATCGTCCCGGG 129

```

```

AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Direct Submission
JOURNAL   Submitted (30-OCT-2001) Civil and Environmental Engineering,
            University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES   Location/Qualifiers
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                /country="Canada: Nova Scotia"
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Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TAATGTCATCGTCCCGGG 19
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Db 147 TAATGTCATCGTCCCGGG 129

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RESULT 14
AF440851/c
LOCUS      168 bp      DNA      linear      BCT 25-NOV-2001

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Qy 1 TAATGTCATCGTCCCGGG 19
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AUTHORS   Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE     Direct Submission
JOURNAL   Submitted (30-OCT-2001) Civil and Environmental Engineering,
            University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES   Location/Qualifiers
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BASE COUNT 47 a 32 c 49 g 33 t
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Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TAATGTCATCGTCCCGGG 19
    |||||
Db 147 TAATGTCATCGTCCCGGG 129

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```

DEFINITION Uncultured gamma proteobacterium DGGE band ns.st8.e3 16S ribosomal
RNA gene, partial sequence.
ACCESSION AF440834
VERSION AF440834.1 GI:17064106
KEYWORDS
SOURCE uncultured gamma proteobacterium
ORGANISM uncultured gamma proteobacterium
Bacteria; Proteobacteria; Gammaproteobacteria; environmental
samples.
REFERENCE 1 (bases 1 to 168)
AUTHORS Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE Bioremediation Treatment Effects On Microbial Community Structure
In A Crude Oil-Contaminated Coastal Marsh
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 168)
AUTHORS Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-2001) Civil and Environmental Engineering,
University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES
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study conducted at a coastal marsh"
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BASE COUNT 47 a 35 c 51 g 35 t
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Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
Db |||||||||||
147 TAATGTCATCGTCCCGGG 129

RESULT 15
AF440834/C
LOCUS
DEFINITION Uncultured gamma proteobacterium DGGE band ns.st8.bl 16S ribosomal
RNA gene, partial sequence.
ACCESSION AF440834
VERSION AF440834.1 GI:17064089
KEYWORDS
SOURCE uncultured gamma proteobacterium
ORGANISM uncultured gamma proteobacterium
Bacteria; Proteobacteria; Gammaproteobacteria; environmental
samples.
REFERENCE 1 (bases 1 to 170)
AUTHORS Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE Bioremediation Treatment Effects On Microbial Community Structure
In A Crude Oil-Contaminated Coastal Marsh
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 170)
AUTHORS Garcia-Blanco,S., Pruden,A., Suidan,M.T., Venosa,A.D. and Lee,K.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-2001) Civil and Environmental Engineering,
University of Cincinnati, 701 ERC, Cincinnati, OH 45221, USA
FEATURES
Location/Qualifiers
1..170
source
/organism="uncultured gamma proteobacterium"
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/note="un-oiled, nutrient-amended plots in an oil

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BASE COUNT 47 a 36 c 52 g 35 t
ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 170;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGGG 19
Db |||||||||||
147 TAATGTCATCGTCCCGGG 129

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Job time : 71.3884 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2003, 22:24:34 ; Search time 5.79223 Seconds
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8854.845 Million cell updates/sec

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Perfect score: 19
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	19	100.0	19	22 AAC87532	Psychrobacter paci
2	19	100.0	1526	22 AAC87531	Psychrobacter paci
3	16.4	86.3	584	21 AAC76269	Human OREF ORF1824
4	16.4	86.3	1882	21 AAF21914	Human breast and o
5	16.4	86.3	1926	22 ABA06572	Human cDNA SBO ID
6	16.4	86.3	1926	24 ABV83909	Human polynucleoti
7	16.4	86.3	1987	21 ABV23368	NSEQ gene-20 assoc
8	16.4	86.3	1987	24 AAL42464	Human matrix-remod

9	16.4	86.3	1989	21 AAA37044	Human PRO1293 (UNC
10	16.4	86.3	1989	22 AAF54255	DNA encoding prote
11	16.4	86.3	1990	21 AAC58113	Human PRO1293 nucl
12	16.4	86.3	2005	22 AAH13666	Human cDNA sequenc
13	16.4	86.3	2132	21 AAC67985	Human MTC48 nucleo
14	16.4	86.3	2132	21 AAC76236	Human OREF ORF1791
15	16.4	86.3	2252	22 AAD12573	Human protein havi
16	16.4	86.3	2243	25 AB57548	Human SECP-4 cDNA
17	16.4	86.3	2619	25 AB57567	Human SECP-23 cDNA
c 18	16.4	86.3	3152	22 AAX28912	Human immunoglobul
c 19	15.8	83.2	268	25 ABX49528	Bovine EST associa
c 20	15.8	83.2	286	25 ABX36977	Bovine EST associa
c 21	15.8	83.2	286	25 ABX38622	Bovine EST associa
c 22	15.8	83.2	286	25 ABX43845	Bovine EST associa
c 23	15.8	83.2	286	25 ABX45011	Bovine EST associa
c 24	15.8	83.2	286	25 ABX45961	Bovine EST associa
c 25	15.8	83.2	286	25 ABX48337	Bovine EST associa
c 26	15.8	83.2	286	25 ABX48361	Bovine EST associa
c 27	15.8	83.2	287	25 ABX36471	Bovine EST associa
c 28	15.8	83.2	288	25 ABX45976	Bovine EST associa
c 29	15.8	83.2	290	25 ABX45470	Bovine EST associa
c 30	15.8	83.2	291	25 ABX35792	Bovine EST associa
c 31	15.8	83.2	292	25 ABX37207	Bovine EST associa
c 32	15.8	83.2	298	25 ABX37182	Bovine EST associa
c 33	15.8	83.2	298	25 ABX41972	Bovine EST associa
c 34	15.8	83.2	298	25 ABX42439	Bovine EST associa
c 35	15.8	83.2	302	25 ABX45259	Bovine EST associa
c 36	15.8	83.2	302	25 ABX46192	Bovine EST associa
c 37	15.8	83.2	303	25 ABX36021	Bovine EST associa
c 38	15.8	83.2	303	25 ABX37441	Bovine EST associa
c 39	15.8	83.2	310	25 ABX37185	Bovine EST associa
c 40	15.8	83.2	398	25 ABX35085	Bovine EST associa
c 41	15.8	83.2	404	25 ABX37912	Bovine EST associa
c 42	15.8	83.2	800	22 AAH05517	Human cDNA clone (
c 43	15.8	83.2	5504	20 AAX20559	Polynucleotide seq
c 44	15.4	81.1	488	20 AAX29126	Polynucleotide RTP
c 45	15.4	81.1	576	22 AAH67217	C glutamicum codin

ALIGNMENTS

RESULT 1
AAC87532
ID AAC87532 standard; DNA; 19 BP.
XX
XX AAC87532;
XX
XX
DT 13-MAR-2001 (first entry)
XX
XX Psychrobacter pacificensis 16S rDNA probe, SEQ ID NO:2.
DE
XX 16S rDNA; species-specific detection; identification;
KW psychrophilic bacterium; oceanic circulation; Psychrobacter;
KW probe; ss.
XX
XX Psychrobacter pacificensis.
XX
XX WO200071705-A1.
XX
XX 30-NOV-2000.
XX
XX 25-MAY-2000; 2000WO-JP03372.
XX
XX 25-MAY-1999; 99JP-0145342.
XX 30-MAR-2000; 2000WO-JP02045.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PI Maruyama A, Kitamura K, Kurane R;
XX
XX WPI; 2001-025158/03.
XX

PT DNA probe originating from psychrotrophic bacterium applicable in
PT species-specific detection of the microorganism as indication in
PT studying and monitoring its growth and circulation of deep-sea water
PT with sensitivity -
XX
PS Claim 3; Page 10; 37pp; Japanese.
XX
CC The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA
CC sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising
CC part of the Psychrobacter pacificensis 16S rDNA sequence which are used
CC for monitoring the growth of psychrophilic bacteria and the circulation
CC of deep-sea water. Psychrobacter pacificensis is an aerobic,
CC Gram-negative, non-motile, non-spore-forming oxidase-positive bacterium
CC originally isolated from the Japan Trench. The invention also relates to
CC a novel method for detecting or specifically identifying Psychrobacter
CC pacificensis, Psychrobacter glacincola, and related species, or
CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence.
CC The 16S rDNA sequence and derived oligonucleotide probe are useful for
CC the species-specific detection of Psychrobacter pacificensis to study
CC and monitor its growth as an indicator of the circulation of deep-sea
CC water. The method of the invention is rapid, accurate and has high
CC sensitivity, and removes the need to separate and culture the biological
CC materials. The present sequence represents a specifically claimed
CC Psychrobacter pacificensis 16S rDNA oligonucleotide probe.
XX
SQ Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 other;
Query Match 100.0%; Score 19; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAATGTCATCGTCCCGGG 19
Db 1 TAATGTCATCGTCCCGGG 19
RESULT 2
AAC87531/c
ID AAC87531 standard; DNA; 1526 BP.
XX
AC AAC87531;
XX
DT 13-MAR-2001 (first entry)
XX
DE Psychrobacter pacificensis NIBH P2K6 16S rDNA, SEQ ID NO:1.
XX
KW 16S rDNA; species-specific detection; identification;
KW psychrophilic bacterium; oceanic circulation; Psychrobacter;
KW strain NIBH P2K6; ds.
XX
OS Psychrobacter pacificensis.
XX
PN WO200071705-A1.
XX
PD 30-NOV-2000.
XX
PF 25-MAY-2000; 2000WO-JP03372.
XX
PR 25-MAY-1999; 99JP-0145342.
PR 30-MAR-2000; 2000WO-JP02045.
XX
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
XX
PI Maruyama A, Kitamura K, Kurane R;
XX
XX WPI; 2001-025158/03.
DR
XX DNA probe originating from psychrotrophic bacterium applicable in
PT species-specific detection of the microorganism as indication in
PT studying and monitoring its growth and circulation of deep-sea water
PT with sensitivity -
XX
PS Claim 1; Page 30; 37pp; Japanese.

XX
CC The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA
CC sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising
CC part of the Psychrobacter pacificensis 16S rDNA sequence which are used
CC for monitoring the growth of psychrophilic bacteria and the circulation
CC of deep-sea water. Psychrobacter pacificensis is an aerobic,
CC Gram-negative, non-motile, non-spore-forming oxidase-positive bacterium
CC originally isolated from the Japan Trench. The invention also relates to
CC a novel method for detecting or specifically identifying Psychrobacter
CC pacificensis, Psychrobacter glacincola, and related species, or
CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence.
CC The 16S rDNA sequence and derived oligonucleotide probe are useful for
CC the species-specific detection of Psychrobacter pacificensis to study
CC and monitor its growth as an indicator of the circulation of deep-sea
CC water. The method of the invention is rapid, accurate and has high
CC sensitivity, and removes the need to separate and culture the biological
CC materials. The present sequence represents the Psychrobacter
CC pacificensis 16S rDNA.
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SQ Sequence 1526 BP; 401 A; 332 C; 467 G; 323 T; 3 other;
Query Match 100.0%; Score 19; DB 22; Length 1526;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAATGTCATCGTCCCGGG 19
Db 476 TAATGTCATCGTCCCGGG 458
RESULT 3
AAC76269
ID AAC76269 standard; cDNA; 584 BP.
XX
AC AAC76269;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORF1824 polynucleotide sequence SEQ ID NO:3647.
XX
KW Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
XX WPI; 2000-602362/57.

DR P-PSDB; AAB42060.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PT
 PT
 PT
 PS Claim 5; Page 2803; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnaric;
 CC antiproliferative; antiparasitic; antitumor; neuroprotective;
 CC osteoprotective; anticonvulsant; antiarthritic; immunosuppressive;
 CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antineoplastic; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, anti-inflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX
 SQ Sequence 584 BP; 74 A; 232 C; 183 G; 93 T; 2 other;

Query Match 86.3%; Score 16.4; DB 21; Length 584;
 Best Local Similarity 94.4%; Pred. No. 98;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AATGTCATCGTCCCGG 19
 |||||

DB 480 AATGTCATCGTCCCGGAG 497

RESULT 4

AAF21914

ID AAF21914 standard; DNA; 1882 BP.

XX AC AAF21914;

XX DT 27-MAR-2001 (first entry)

XX DE Human breast and ovarian cancer associated antigen gene SEQ ID 301.

XX KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KW nontropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antineoplastic; antitumor; antitumor; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease; ds.

XX OS Homo sapiens.

XX PN WO200055173-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US05881.

XX PR 12-MAR-1999; 99US-0124270.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX WPI; 2000-611515/58.

DR P-PSDB; AAB59011.

XX New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention,
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular
 PT disorders and neurological diseases -
 PT
 XX Claim 1; Page 712-713; 1299pp; English.

PS Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;
 CC nontropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 CC antidiabetic; antineoplastic; antitumor; antitumor; anticonvulsant;
 CC antibacterial; antifungal; antiparasitic and cardiac activity. The
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,
 CC particularly breast and ovarian cancer. The nucleic acid sequences,
 CC proteins, agonists and antagonists may also be used in the diagnosis,
 CC prevention and treatment of immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; cardiovascular disorders such as
 CC myocardial ischaemia; wound healing; neurological diseases such as
 CC cerebral anoxia and epilepsy; and infectious diseases.

XX
 SQ Sequence 1882 BP; 383 A; 616 C; 527 G; 350 T; 6 other;

Query Match 86.3%; Score 16.4; DB 21; Length 1882;
 Best Local Similarity 94.4%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AATGTCATCGTCCCGG 19
 |||||

DB 529 AATGTCATCGTCCCGGAG 546

RESULT 5

ABA06572

ID ABA06572 standard; cDNA; 1926 BP.

XX AC ABA06572;

XX DT 10-JAN-2002 (first entry)

XX DE Human cDNA SEQ ID NO: 238.

XX KW Human; gene therapy; neural disorder; immune system disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; inflammation; ss.

XX OS Homo sapiens.

XX PN WO200154474-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01349.

XX PR 31-JAN-2000; 2000US-179065P.

XX PR 04-FEB-2000; 2000US-180628P.

XX PR 24-FEB-2000; 2000US-184664P.

XX PR 02-MAR-2000; 2000US-186350P.

XX PR 16-MAR-2000; 2000US-189874P.

XX PR 17-MAR-2000; 2000US-190076P.

XX PR 18-APR-2000; 2000US-198123P.

XX PR 19-MAY-2000; 2000US-205515P.

PR 07-JUN-2000; 2000US-209457P.
PR 28-JUN-2000; 2000US-214886P.
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PR 14-JUL-2000; 2000US-218290P.
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PR 01-SEP-2000; 2000US-229287P.
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PR 08-SEP-2000; 2000US-232080P.
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PR 12-SEP-2000; 2000US-231968P.
PR 14-SEP-2000; 2000US-232397P.
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PR 21-SEP-2000; 2000US-234223P.
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PR 29-SEP-2000; 2000US-236370P.
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PR 20-OCT-2000; 2000US-241221P.

PR 20-OCT-2000; 2000US-241785P.
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PR 20-OCT-2000; 2000US-241826P.
PR 01-NOV-2000; 2000US-244617P.
PR 08-NOV-2000; 2000US-246474P.
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PR 08-NOV-2000; 2000US-246476P.
PR 08-NOV-2000; 2000US-246477P.
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PR 08-NOV-2000; 2000US-246523P.
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PR 08-NOV-2000; 2000US-246609P.
PR 08-NOV-2000; 2000US-246610P.
PR 08-NOV-2000; 2000US-246611P.
PR 08-NOV-2000; 2000US-246613P.
PR 17-NOV-2000; 2000US-249207P.
PR 17-NOV-2000; 2000US-249208P.
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PR 17-NOV-2000; 2000US-249212P.
PR 17-NOV-2000; 2000US-249213P.
PR 17-NOV-2000; 2000US-249214P.
PR 17-NOV-2000; 2000US-249215P.
PR 17-NOV-2000; 2000US-249216P.
PR 17-NOV-2000; 2000US-249217P.
PR 17-NOV-2000; 2000US-249218P.
PR 17-NOV-2000; 2000US-249244P.
PR 17-NOV-2000; 2000US-249245P.
PR 17-NOV-2000; 2000US-249246P.
PR 17-NOV-2000; 2000US-249264P.
PR 17-NOV-2000; 2000US-249265P.
PR 17-NOV-2000; 2000US-249297P.
PR 17-NOV-2000; 2000US-249299P.
PR 17-NOV-2000; 2000US-249300P.
PR 01-DEC-2000; 2000US-250160P.
PR 01-DEC-2000; 2000US-250391P.
PR 05-DEC-2000; 2000US-251030P.
PR 05-DEC-2000; 2000US-251988P.
PR 05-DEC-2000; 2000US-256719P.
PR 06-DEC-2000; 2000US-251479P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
PR 08-DEC-2000; 2000US-251899P.
PR 08-DEC-2000; 2000US-251990P.
PR 11-DEC-2000; 2000US-254097P.
PR 05-JAN-2001; 2001US-259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX
XX WPI; 2001-476161/51.
XX P-PSDB; ABB10350.
XX
XX Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition -
XX
XX Claim 1; SEQ ID NO: 238; 859pp + Sequence Listing; English.
XX
XX The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence

CC is a cDNA of the invention.

XX Sequence 1926 BP; 395 A; 654 C; 536 G; 341 T; 0 other;

SO Query Match 86.3%; Score 16.4; DB 22; Length 1926;

Best Local Similarity 94.4%; Pred. No. 1.1e-02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AATGTCATCGTCCCGGG 19

|||||

Db 573 AATGTCATCGTCCCGAG 590

RESULT 6

ABV83909

ID ABV83909 standard; cDNA; 1926 BP.

XX

AC ABV83909;

XX

DT 09-DEC-2002 (first entry)

XX

DE Human polynucleotide SEQ ID NO 238.

XX

XX Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischlicking; antianemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antinflammatory;
KW antidiabetic; antidiabetic; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
XX gene; ss.

XX

OS Homo sapiens.

XX

PN US2002090672-A1.

XX

PD 11-JUL-2002.

XX

PF 17-JAN-2001; 2001US-0764853.

XX

PR 31-JAN-2000; 2000US-179065P.

PR

PR 04-FEB-2000; 2000US-180628P.

PR

PR 28-JUN-2000; 2000US-214886P.

PR

PR 07-JUL-2000; 2000US-216647P.

PR

PR 07-JUL-2000; 2000US-216880P.

PR

PR 11-JUL-2000; 2000US-217487P.

PR

PR 11-JUL-2000; 2000US-217496P.

PR

PR 14-JUL-2000; 2000US-218290P.

PR

PR 26-JUL-2000; 2000US-220963P.

PR

PR 26-JUL-2000; 2000US-220964P.

PR

PR 14-AUG-2000; 2000US-224518P.

PR

PR 14-AUG-2000; 2000US-224519P.

PR

PR 14-AUG-2000; 2000US-225267P.

PR

PR 14-AUG-2000; 2000US-225268P.

PR

PR 14-AUG-2000; 2000US-225270P.

PR

PR 14-AUG-2000; 2000US-225447P.

PR

PR 14-AUG-2000; 2000US-225757P.

PR

PR 14-AUG-2000; 2000US-225758P.

PR

PR 30-AUG-2000; 2000US-228924P.

PR

PR 01-SEP-2000; 2000US-229287P.

PR

PR 01-SEP-2000; 2000US-229343P.

PR

PR 01-SEP-2000; 2000US-229344P.

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PR 01-SEP-2000; 2000US-229345P.

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PR 05-SEP-2000; 2000US-229509P.

PR

PR 05-SEP-2000; 2000US-229513P.

PR

PR 08-SEP-2000; 2000US-231413P.

PR

PR 21-SEP-2000; 2000US-234223P.

PR

PR 21-SEP-2000; 2000US-234274P.

PR

PR 25-SEP-2000; 2000US-234997P.

PR

PR 27-SEP-2000; 2000US-235834P.

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PR 29-SEP-2000; 2000US-236327P.

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PR 29-SEP-2000; 2000US-236367P.

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PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239935P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.

PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX

PI Rosen CA, Ruben SM, Barash SC;

XX

XX WPI: 2002-681727/73.

DR

DR P-PSDB; ABP66937.

XX

PT Novel polypeptide useful for diagnosis, prognosis, prevention, and
PT treatment of immune, hyperproliferative, renal, respiratory,
PT cardiovascular, reproductive, endocrine, gastrointestinal and
PT neurological disorders

XX

PS Claim 1; SEQ ID NO 238; 369pp + Sequence Listing; English.

XX

CC The invention relates to novel genes (ABV83682-ABV84101) and proteins
(ABP66710-ABP67129) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 1926 BP; 395 A; 654 C; 536 G; 341 T; 0 other;

Query Match 86.3%; Score 16.4; DB 24; Length 1926;

Best Local Similarity 94.4%; Pred. No. 1.1e-02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AATGTCATCGTCCCGGG 19

|||||

Db 573 AATGTCATCGTCCCGAG 590

RESULT 7

AAZ52368

ID AAZ52368 standard; cDNA; 1987 BP.

XX

AC AAZ52368;

XX

DT 24-JUL-2000 (first entry)

XX

DE NSEQ gene-20 associated with matrix remodelling.

XX NSEQ gene; matrix-remodeling gene; Incyte clone 3948614; cancer;
 KW matrix-remodeling disease; cardiomyopathy; arthritis; angiogenesis;
 KW diabetic necrosis; atherosclerosis; fibrosis; ulceration; cytostatic;
 KW cardioactive; antiarthritic; angiogenic; antiarteriosclerotic;
 KW antiulcer; ss.
 XX Homo sapiens.
 OS
 XX WO200021986-A2.
 PN
 XX 20-APR-2000.
 PD
 XX 06-OCT-1999; 99WO-US23315.
 PF
 XX 09-OCT-1998; 98US-0169289.
 PR
 XX (INCY-) INCYTE PHARM INC.
 PA Walker MG, Volkmath W, Klingler TM;
 XX WPI; 2000-317934/27.
 PI
 XX Protein co-expressed with matrix-remodeling proteins, useful in the
 PT diagnosis and treatment of cancer, cardiomyopathy, arthritis,
 PT angiogenesis, diabetic necrosis, atherosclerosis, fibrosis, and
 PT ulceration.
 XX
 XX Claim 1; Page 51-52; 55pp; English.
 PS
 XX The present sequence is NSEQ gene that is co-expressed with one or more
 CC known matrix-remodeling genes in a number of biological samples using an
 CC expression vector. This sequence was identified from the
 CC Incyte clone 3948614. The gene, protein, and antibody sequences can be
 CC used in the diagnosis, and treatment or prevention of a disease
 CC associated with its altered expression. The diseases that can be treated
 CC are matrix-remodeling diseases, including cancer, cardiomyopathy,
 CC arthritis, angiogenesis, diabetic necrosis, atherosclerosis, fibrosis,
 CC and ulceration.
 XX
 XX Sequence 1987 BP; 345 A; 597 C; 579 G; 366 T; 0 other;
 SQ
 Query Match 86.3%; Score 16.4; DB 21; Length 1987;
 Best Local Similarity 94.4%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AATGTCATCGTCCCCGG 19
 DB 716 AATGTCATCGTCCCCGAG 733
 RESULT 8
 ID AAL42464 standard; DNA; 1987 BP.
 XX AAL42464;
 AC
 XX 11-JUL-2002 (first entry)
 DT
 XX Human matrix-remodeling-associated nucleotide 20.
 DE
 XX Human; ds; matrix-remodeling gene; extracellular matrix; gene;
 KW matrix-remodeling-associated nucleotide; screening;
 KW matrix remodelling-associated disease; angiogenesis; arthritis;
 KW atherosclerosis; cancer; cardiomyopathy; diabetic necrosis; fibrosis;
 KW ulceration.
 XX
 XX Homo sapiens.
 OS
 XX US2002019000-A1.
 PN
 XX 14-FEB-2002.
 PD
 XX

PF 26-MAR-2001; 2001US-0818143.
 XX
 PR 09-OCT-1998; 98US-0169289.
 XX (WALK/) WALKER M G.
 PA (VOLK/) VOLKMAT W.
 PA (KLIN/) KLINGLER T M.
 XX Walker MG, Volkmath W, Klingler TM;
 PI WPI; 2002-338319/37.
 DR
 XX New isolated polynucleotide coexpressed with matrix-remodeling genes,
 PT useful in diagnosis, prognosis, prevention and treatment of diseases
 PT associated with matrix-remodeling such as angiogenesis, arthritis and
 PT cancer.
 XX
 XX Claim 2; Page 36-37; 63pp; English.
 PS
 XX The invention comprises human nucleotide sequences which are co-expressed
 CC with matrix-remodeling genes. Matrix-remodeling is associated with the
 CC construction, destruction and reorganisation of extracellular matrix
 CC components. The matrix-remodeling-associated nucleotides of the invention
 CC are useful for screening for and purifying ligands that specifically bind
 CC to the nucleotides of the invention. The matrix-remodelling-associated
 CC nucleotides of the invention are also useful in the diagnosis, prognosis,
 CC prevention, treatment and evaluation of therapies for diseases associated
 CC with matrix remodelling (e.g. angiogenesis, arthritis, atherosclerosis,
 CC cancer, cardiomyopathy, diabetic necrosis, fibrosis and ulceration). The
 CC present DNA sequence represents a human matrix-remodeling-associated
 CC nucleotide of the invention.
 XX
 XX Sequence 1987 BP; 345 A; 597 C; 579 G; 366 T; 0 other;
 SQ
 Query Match 86.3%; Score 16.4; DB 24; Length 1987;
 Best Local Similarity 94.4%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AATGTCATCGTCCCCGG 19
 DB 716 AATGTCATCGTCCCCGAG 733
 RESULT 9
 ID AAA37044 standard; cDNA; 1989 BP.
 XX AAA37044;
 AC
 XX 08-AUG-2000 (first entry)
 DT
 XX Human PRC1293 (UNQ662) cDNA sequence SEQ ID NO:76.
 DE
 XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
 KW ss.
 KW
 XX Homo sapiens.
 OS
 XX WO2000012708-A2.
 PN
 XX 09-MAR-2000.
 PD
 XX 01-SEP-1999; 99WO-US20111.
 PF
 XX 01-SEP-1998; 98US-0098716.
 PR 01-SEP-1998; 98US-0098749.
 PR 01-SEP-1998; 98US-0098750.
 PR 02-SEP-1998; 98US-0098803.
 PR 02-SEP-1998; 98US-0098821.
 PR 02-SEP-1998; 98US-0098843.
 PR 09-SEP-1998; 98US-0099536.
 PR 09-SEP-1998; 98US-0099596.

PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
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PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 17-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.

PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0106500.
PR 30-OCT-1998; 98US-0106464.
PR 30-OCT-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108859.
PR 18-NOV-1998; 98US-0108904.

XX
PA (GETH) GENENTECH INC.
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CX, Wood WI;
XX
XX WPI; 2000-237871/20.
DR P-PSDB; AAY99362.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
FT small molecule inhibitors of the relevant receptor/ligand interactions
XX
PS Claim 2; Fig 45; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
XX
SQ Sequence 1989 BP; 340 A; 693 C; 586 G; 370 T; 0 other;

Query Match 86.3%; Score 16.4; DB 21; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATGTCCTCCGGG 19
|||||||

Db 715 AATGTCATCGTCCCGAG 732

RESULT 10
AAF54255
ID AAF54255 standard; DNA; 1989 BP.
XX
XX AAF54255;
AC
XX
XX 02-APR-2001 (first entry)
DT
XX
XX DNA encoding protein of the invention #23.
DE
XX
KW Secreted; transmembrane; gene therapy; ss.
XX
XX Unidentified.
OS
XX
XX W0200078961-AL.
FN
XX
XX 28-DEC-2000.
PD
XX
XX 18-FEB-2000; 2000WO-US04342.
PF
XX
XX 23-JUN-1999; 99US-0141037.
PR
XX
XX 20-JUL-1999; 99US-0144758.
PR
XX
XX 26-JUL-1999; 99US-0145698.
PR
XX
XX 01-SEP-1999; 99WO-US20111.
PR
XX
XX 29-OCT-1999; 99US-0162506.
PR
XX
XX 30-NOV-1999; 99WO-US28313.
PR
XX
XX 02-DEC-1999; 99WO-US28551.
PR
XX
XX 16-DEC-1999; 99WO-US30095.
PR
XX
XX 05-JAN-2000; 2000WO-US00219.
PR
XX
XX 06-JAN-2000; 2000WO-US00376.
XX
XX
XX (GETH) GENENTECH INC.
FA
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI
XX
XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI
XX
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI
XX
XX Watanabe CK, Williams PM, Wood WI;
XX
XX
XX WPI; 2001-071395/08.
DR
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
PT
XX
XX useful as hybridization probes, in chromosome and gene mapping and gene
PT
XX
XX therapy.
PT
XX
XX Claim 2; Fig 45; 787pp; English.
PS
XX
XX The present invention relates to secreted and transmembrane proteins.
CC
XX
XX These proteins and the DNA encoding them may be used as hybridization
CC
XX
XX probes, in chromosome and gene mapping and in the generation of
CC
XX
XX anti-sense RNA and DNA. They may also be used to generate either
CC
XX
XX transgenic animals or knockout animals which are in turn useful for
CC
XX
XX development and screening of therapeutically useful reagents.
CC
XX
XX The nucleic acids may also be used in gene therapy.
CC
XX
XX Sequence 1989 BP; 340 A; 693 C; 586 G; 370 T; 0 other;
SQ

Query Match 86.3%; Score 16.4; DB 22; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19
|||||

Db 715 AATGTCATCGTCCCGAG 732

RESULT 11
AAC58113
ID AAC58113 standard; cDNA; 1990 BP.
XX
XX AAC58113;

XX 25-JAN-2001 (first entry)
DT
XX
XX Human PRO1293 nucleotide sequence SEQ ID NO:30.
DE
XX
XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
KW
XX
XX identification; tumorigenesis; anticancer; detection; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX W0200053750-AL.
FN
XX
XX 14-SEP-2000.
PD
XX
XX 02-DEC-1999; 99WO-US28551.
PF
XX
XX 08-MAR-1999; 99WO-US05028.
PR
XX
XX 01-SEP-1999; 99WO-US20111.
PR
XX
XX 23-OCT-1999; 99US-0162506.
PR
XX
XX 30-NOV-1999; 99WO-US28313.
PR
XX
XX 01-DEC-1999; 99WO-US28634.
PR
XX
XX (GETH) GENENTECH INC.
FA
XX
XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
PI
XX
XX WPI; 2000-594320/56.
DR
XX
XX P-PSDB; AAB24031.
DR
XX
XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT
XX
XX the growth of tumors in mammals, and to identify inhibitors of PRO
PT
XX
XX polypeptide activity or expression.
PT
XX
XX Claim 50; Fig 21; 226pp; English.
PS
XX
XX The present invention describes an antibody that binds to a human
CC
XX
XX protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;
CC
XX
XX PRO3434; PRO1927; PRO3567; PRO1293; PRO1303; PRO4344; PRO4354;
CC
XX
XX PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has
CC
XX
XX anticancer activity and can be used to diagnose tumours in mammals, by
CC
XX
XX detecting complex formation when the antibody is contacted with test
CC
XX
XX cells. Increased expression of genes encoding (I) can also be detected
CC
XX
XX to diagnose tumours. Agents which inhibit the activity of (I),
CC
XX
XX especially the antibodies, or an antisense oligonucleotide which
CC
XX
XX hybridises to genes encoding (I), can be used to inhibit tumour growth,
CC
XX
XX preferably by inducing cell death. Methods from the present invention
CC
XX
XX can be used to identify compounds which inhibit the biological activity
CC
XX
XX of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation
CC
XX
XX probes used in examples from the present invention for human PRO
CC
XX
XX sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human
CC
XX
XX PRO polynucleotide and protein sequences given in the exemplification of
CC
XX
XX the present invention.
CC
XX
XX Sequence 1990 BP; 341 A; 693 C; 586 G; 370 T; 0 other;
SQ

Query Match 86.3%; Score 16.4; DB 21; Length 1990;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19
|||||

Db 715 AATGTCATCGTCCCGAG 732

RESULT 12
AAH13666
ID AAH13666 standard; cDNA; 2005 BP.
XX
XX AAH13666;
AC
XX
XX 26-JUN-2001 (first entry)
DT
XX
XX Human cDNA sequence SEQ ID NO:10519.
DE

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 KW Homo sapiens.
 OS BP1074617-A2.
 PN 07-FEB-2001.
 PD 28-JUL-2000; 2000EP-0116126.
 PF 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX (HELI-) HELIX RES INST.
 PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR WPI; 2001-318749/34.
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX Claim 8; SEQ ID 10519; 2537pp + CD ROM; English.
 XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB93893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX Sequence 2005 BP; 318 A; 700 C; 626 G; 361 T; 0 other;
 SQ Query Match 86.3%; Score 16.4; DB 22; Length 2005;
 Best Local Similarity 94.4%; Pred. No. 1.1e-02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AATGTCATGTCCTCCGGG 19
 DB 1025 AATGTCATGTCCTCCGGG 1042
 RESULT 13
 AAC67985
 ID AAC67985 standard; cDNA; 2132 BP.
 XX AAC67985;
 AC
 DT 20-FEB-2001 (first entry)
 XX

DE Human MTC48 nucleotide sequence.
 KW Human; cytostatic; metastatic thyroid cancer; MTC; thyroid carcinoma; ss.
 XX Homo sapiens.
 OS WO200063438-A2.
 PN 26-OCT-2000.
 PD 20-APR-2000; 2000WO-US10729.
 PF 20-APR-1999; 99US-0130123.
 PR 30-MAR-2000; 2000US-0193203.
 PR 19-APR-2000; 2000US-0552322.
 XX (CURA-) CURAGEN CORP.
 PA Gould-Rothberg BE, Rastelli L;
 PI WPI; 2000-565252/64.
 DR P-PSDB; AAB36107.
 XX Categorizing, diagnosing or assessing the prognosis of thyroid
 PT carcinoma by measuring the expression levels of MTC (metastatic thyroid
 PT cancer) genes -
 XX Claim 1; Page 32-33; 105pp; English.
 XX The present sequence encodes a novel metastatic thyroid cancer (MTC)
 CC protein. A method of categorising, diagnosing or assessing the prognosis
 CC of thyroid carcinoma by measuring the expression levels of MTC genes is
 CC disclosed. The MTC genes are differentially expressed in metastatic
 CC thyroid cancer when compared to non-metastatic thyroid cancer. An
 CC agent that decreases the expression or activity of one or more MTC genes
 CC may be administered to treat metastatic carcinoma. Allele-specific
 CC oligonucleotide probes that hybridise to an MTC polynucleotide at a
 CC polymorphic site may be used to determine whether a subject suffers from
 CC or is at risk of metastatic thyroid carcinoma.
 XX Sequence 2132 BP; 360 A; 751 C; 644 G; 377 T; 0 other;
 SQ Query Match 86.3%; Score 16.4; DB 21; Length 2132;
 Best Local Similarity 94.4%; Pred. No. 1.1e-02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AATGTCATGTCCTCCGGG 19
 DB 844 AATGTCATGTCCTCCGGG 861
 RESULT 14
 AAC76236
 ID AAC76236 standard; cDNA; 2132 BP.
 XX AAC76236;
 AC
 DT 08-FEB-2001 (first entry)
 XX Human OREF791 polynucleotide sequence SEQ ID NO:3581.
 DE Human; open reading frame; OREF; detection; cytostatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 XX

KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.
 OS Homo sapiens.
 XX WO2000058473-A2.
 XX 05-OCT-2000.
 XX 31-MAR-2000; 2000WO-US08621.
 XX 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX (CURA-) CURAGEN CORP.
 XX Shimkets RA, Leach M;
 XX WPI; 2000-602362/57.
 DR P-PSDB; AAB42027.
 XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX Claim 5; Page 2741-2743; 5507pp; English.
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipapillary; antiparkinsonian; neotropic; neuroprotective;
 CC osteoparitic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection; malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX Sequence 2132 BP; 360 A; 751 C; 642 G; 377 T; 2 other;
 SQ Query Match 86.3%; Score 16.4; DB 21; Length 2132;
 Best Local Similarity 94.4%; Pred. No. 1.le+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AATGTCATCGTCCCGG 19
 |||||
 Db 846 AATGTCATCGTCCCGG 863
 |||||
 RESULT 15
 AAD12573
 ID AAD12573 standard; cDNA; 2252 BP.
 XX AAD12573;
 AC AAD12573;
 XX 25-SEP-2001 (first entry)
 XX Human protein having hydrophobic domain encoding cDNA clone HP10769.
 DE Human; hydrophobic domain; gene therapy; nutritional supplement;
 KW Human; hydrophobic domain; gene therapy; nutritional supplement;

KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 KW hematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
 KW contraceptive; antifertility; antiinflammatory; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX 12..1340
 FT /tag= a
 FT /product= "Human protein having hydrophobic domain"
 FT /note= "CDS is specifically is claimed in claim 3"
 XX WO200149728-A2.
 XX 12-JUL-2001.
 XX 28-DEC-2000; 2000WO-JP09359.
 XX 06-JAN-2000; 2000JP-0000585.
 PR 06-JAN-2000; 2000JP-0000588.
 PR 11-JAN-2000; 2000JP-0002299.
 PR 03-FEB-2000; 2000JP-0026862.
 PR 03-MAR-2000; 2000JP-0058367.
 XX (PROT-) PROTEGENE INC.
 XX (SAGA) SAGAMI CHEM RES CENT.
 XX Kato S, Kimura T;
 XX WPI; 2001-419355/44.
 DR P-PSDB; AAE06578.
 XX Human proteins with hydrophobic domains and the nucleic acids encoding
 PT them, useful for preventing diagnosing and treating e.g. cancer,
 PT Alzheimer's and inflammation -
 XX Claim 4; Page 282-286; 563pp; English.
 CC The present sequence is human protein with hydrophobic domain encoding
 CC cDNA clone HP10769. The polynucleotide and polypeptide of the invention
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The polynucleotides
 CC may be used to produce the polypeptide, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. The
 CC polynucleotides and its complementary sequences may also be used as DNA
 CC probes in diagnostic assays and also used in gene therapy. The
 CC polypeptides may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of polypeptide expression and
 CC activity. The polypeptides and nucleic acids may be used as nutritional
 CC supplements, to modulate cytokine and cell proliferation activity, to
 CC modulate immune stimulation or suppression (e.g. for the treatment of
 CC microbial infections and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
 CC hematopoiesis, to modulate tissue growth activity (e.g. for the
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
 CC disease), to modulate activin and inhibin activity (e.g. for controlling
 CC fertility), to modulate chemotactic and chemokinetic activity, to
 CC modulate haemostatic and thrombolytic activity, to modulate receptor
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.
 XX Sequence 2252 BP; 349 A; 798 C; 694 G; 411 T; 0 other;
 SQ Query Match 86.3%; Score 16.4; DB 22; Length 2252;
 Best Local Similarity 94.4%; Pred. No. 1.le+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AATGTCATCGTCCCGG 19
 |||||
 Db 993 AATGTCATCGTCCCGG 1010
 |||||

Search completed: August 20, 2003, 02:03:59
Job time : 6.79223 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 01:43:45 ; Search time 43.2142 Seconds
(without alignments)
10685.946 Million cell updates/sec

Title: US-09-979-558A-2

Perfect score: 19
Sequence: 1 taatgtcatgtcccgagg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_plo:*

20: em_gss_prt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vri:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	16.4	86.3	337	14	W92952
c 2	16.4	86.3	340	9	AA037563
c 3	16.4	86.3	369	14	W45082
c 4	16.4	86.3	513	9	AA115144

c	5	16.4	86.3	533	9	AI817726
c	6	16.4	86.3	537	14	W16559
c	7	16.4	86.3	539	9	AI772402
c	8	16.4	86.3	554	12	BI627185
c	9	16.4	86.3	562	10	AW963853
c	10	16.4	86.3	595	10	BF342569
c	11	16.4	86.3	623	9	AL680804
c	12	16.4	86.3	682	10	BG127540
c	13	16.4	86.3	768	12	BI758715
c	14	16.4	86.3	799	12	BI754114
c	15	16.4	86.3	903	13	BQ881886
c	16	16.4	86.3	957	13	BQ717752
c	17	16.4	86.3	1060	13	BU134659
c	18	16.4	86.3	1129	12	BM924224
c	19	16.4	86.3	1201	9	AL553402
c	20	16.4	86.3	1201	13	BA39049
c	21	16.4	86.3	1987	10	AW888223
c	22	16.4	86.3	435	9	AI329817
c	23	16.4	86.3	511	9	AI397616
c	24	16.4	86.3	517	9	AI186852
c	25	16.4	86.3	639	9	AV849197
c	26	16.4	86.3	648	9	AI398536
c	27	16.4	86.3	686	9	AV849138
c	28	16.4	86.3	701	28	BH954585
c	29	16.4	86.3	709	28	BH954543
c	30	16.4	86.3	831	28	BH423226
c	31	15.8	83.2	192	29	BZ672389
c	32	15.8	83.2	215	9	AV025145
c	33	15.8	83.2	243	12	BM106925
c	34	15.8	83.2	289	13	BQ640964
c	35	15.8	83.2	300	9	AU231776
c	36	15.8	83.2	300	9	AU231871
c	37	15.8	83.2	300	9	AV181313
c	38	15.8	83.2	300	14	C55494
c	39	15.8	83.2	300	14	C57763
c	40	15.8	83.2	320	28	BZ138443
c	41	15.8	83.2	324	28	BZ137662
c	42	15.8	83.2	347	14	CB225018
c	43	15.8	83.2	350	9	AU233974
c	44	15.8	83.2	353	9	AU278375
c	45	15.8	83.2	390	28	BH777025

ALIGNMENTS

RESULT 1
W92952/c

LOCUS

DEFINITION

W92952

W92952

W92952

W92952

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W92952

W92952

W92952

W92952

W92952

W92952

W92952

W92952

W92952

W92952 337 bp mRNA linear EST 25-NOV-1996

z492e10.r1 Soares_fetal_heart_NbHHL9W Homo sapiens cDNA clone

IMAGE:356970 5' similar to contains element MER22 repetitive

element ;, mRNA sequence.

W92952 GI:1422104

W92952

W92952

W92952

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W92952

W92952

W92952

W92952

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 337)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman

, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston

, R., Williamson, A., Wohldmann, P., and Wilson, R.

The WashU-Merck EST Project

Unpublished

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estwatson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 998 Std Error: 0.00
Seq primer: mob.REGA+ET

High quality sequence stop: 279.
Location/Qualifiers

FEATURES

source

```

1. .337
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1273514"
/db_xref="taxon:9606"
/clone="IMAGE:356970"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NbHL19W"
/notes="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site1: Not I; Site2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACATCTGAAGTGGAGCGCCGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."
BASE COUNT      63 a  94 c 111 g  67 t   2 others
ORIGIN
Query Match      86.3%; Score 16.4; DB 14; Length 337;
Best Local Similarity 94.4%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 AATGTCATCGTCCCGGG 19
|||||
Db  273 AATGTCATCGTCCCGAG 256

RESULT 2
AA037563/C
LOCUS      AA037563      340 bp  mRNA  linear  EST 10-MAY-1997
DEFINITION zk34a03.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:484684 5', mRNA sequence.
ACCESSION  AA037563
VERSION     AA037563.1 GI:1512663
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 340)
AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Treviskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
79044478
8889549
PUBMED
COMMENT    Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 597 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 121.

```

FEATURES

source

```

Location/Qualifiers
1. .340
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3758398"
/db_xref="taxon:9606"
/clone="IMAGE:484684"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/notes="Organ: uterus; Vector: pT7T3-Pac; Site1: Not I;
Site2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AATGGAAGAAATGCGCGCCCTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
BASE COUNT      54 a 109 c 115 g  53 t   9 others
ORIGIN
Query Match      86.3%; Score 16.4; DB 9; Length 340;
Best Local Similarity 94.4%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 AATGTCATCGTCCCGGG 19
|||||
Db  35 AATGTCATCGTCCCGAG 18

RESULT 3
W45082
LOCUS      W45082      369 bp  mRNA  linear  EST 10-OCT-1996
DEFINITION zc2ig10.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
clone IMAGE:323010 5', mRNA sequence.
ACCESSION  W45082
VERSION     W45082.1 GI:1329213
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 369)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treviskis,E., Waterston
,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1423 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 326.
Location/Qualifiers
1. .369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1254522"
/db_xref="taxon:9606"
/clone="IMAGE:323010"
/tissue_type="Senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/notes="Vector: pT7T3D (Pharmacia) with a modified

```


W16559 537 bp mRNA linear EST 29-APR-1996
LOCUS zbl1b12.r1 Soares_fetal_lung_NbHL19 Homo sapiens cDNA clone
DEFINITION IMAGE:301727 5' similar to contains element MSRI repetitive element
 ; mRNA sequence.
ACCESSION W16559
VERSION W16559.1 GI:1290941
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 537)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 , M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
 , R., Williamson, A., Wohldmann, P. and Wilson, R.
 The WashU-Merck EST Project
TITLE Unpublished
JOURNAL Contact: Wilson RK
COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
FEATURES Seq primer: ETPRimer
 High quality sequence stop: 342.
 Location/Qualifiers
 1..537
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:1246658"
 /db_xref="taxon:9606"
 /clone="IMAGE:301727"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares_fetal_lung_NbHL19"
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer
 15'-TGTACCAATCGAGTGGAGCGCCGCAATTTTTTTTTTTT-3',
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NbHL19."
BASE COUNT 115 a 137 c 164 g 112 t 9 others
ORIGIN
 Query Match 86.3%; Score 16.4; DB 14; Length 537;
 Best Local Similarity 94.4%; Pred. No. 7.le+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AATGTCATCGTCCCGGG 19
 |||||
 Db 18 AATGTCATCGTCCCGAG 35
RESULT 7
LOCUS AI772402 539 bp mRNA linear EST 18-MAY-2001
DEFINITION EST253502 tomato resistant, Cornell Lycopersicon esculentum cDNA
 clone cLER2H9, mRNA sequence.
ACCESSION AI772402
VERSION AI772402.1 GI:5270443
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 539)
AUTHORS D'Ascenzo, M., He, X., Lyman, J., Materu, A.L., Vision, T., Holt, J.E.,
 Liang, F., Upton, J., Roaning, C.M., Craven, M.B., Fujii, C.Y., Bowman
 , C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
 Giovannoni, J.J. and Martin, G.B.
 Generation of ESTs from Pseudomonas resistant tomato
 Unpublished
TITLE Contact: CUGI
JOURNAL Clemson University Genomics Institute
COMMENT Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html
 5 prime sequence.
FEATURES Location/Qualifiers
 1..539
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="R11-12 (35S::Pto in Rio Grande x Money Maker)"
 /db_xref="taxon:4081"
 /clone="CLER2H9"
 /tissue_type="leaf"
 /dev_stage="4-week old"
 /lab_host="SOLR"
 /clone_lib="tomato resistant, Cornell"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; cLER - Tomato Pseudomonas Resistant EST Library.
 Directionally cloned cDNAs inserted into pBluescript SK(-
) at 5' end with EcoRI and 3' end with XhoI site."
BASE COUNT 158 a 118 c 127 g 135 t 1 others
ORIGIN
 Query Match 86.3%; Score 16.4; DB 9; Length 539;
 Best Local Similarity 94.4%; Pred. No. 7.le+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AATGTCATCGTCCCGGG 19
 |||||
 Db 438 AATGTCATCGTCCCGGG 455
RESULT 8
LOCUS BI627185 554 bp mRNA linear EST 07-SEP-2001
DEFINITION RH86421.5prime RH Drosophila melanogaster normalized Head pFlc-1
 Drosophila melanogaster cDNA clone RH86421.5 similar to igl:
 FBan0018285 GO:[ligand binding or carrier (GO:0005488)]; calmodulin
 binding (GO:0005516)] located on: 2R 51E5-51E7;: 08/24/2001, mRNA
 sequence.
ACCESSION BI627185
VERSION BI627185.1 GI:15522710
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 554)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
 , J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
 , R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
 Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
 Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celnikier, S. and Rubin
 , G.M.
TITLE BDGP/HMI RH Drosophila EST Project
JOURNAL Unpublished
COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Plate: RH.684 row: B column: 9

High quality sequence stop: 462.

FEATURES

source

1. .554
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RH68421"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/clone_lib="RH Drosophila melanogaster normalized Head
pFlc-1"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
BASE COUNT 177 a 136 c 142 g 99 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 554;
Best Local Similarity 94.4%; Pred. No. 7.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGGG 19
|||||
Db 473 AATGTCATCGTCCCGGG 456

RESULT 9
AW963853
LOCUS AW963853 562 bp mRNA linear EST 01-JUN-2000
DEFINITION EST375926 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION AW963853
VERSION AW963853.1 GI:8153689
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 562)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 194
Seq primer: Reverse.

FEATURES

source

1. .562
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE"
/note="vector: pBluescriptSKM"
BASE COUNT 114 a 180 c 159 g 109 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 562;
Best Local Similarity 94.4%; Pred. No. 7.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGGG 19
|||||
Db 45 AATGTCATCGTCCCGGG 62

RESULT 10

BF342569

LOCUS

DEFINITION

BF342569

ACCESSION

BF342569

VERSION

BF342569.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 595)

AUTHORS

NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9411 row: j column: 24

High quality sequence stop: 589.

FEATURES

source

1. 595
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4149623"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI-CGAP-Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP Library."
BASE COUNT 82 a 226 c 195 g 92 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 595;
Best Local Similarity 94.4%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGGG 19
|||||
Db 487 AATGTCATCGTCCCGGG 504

RESULT 11

AL680804/c

LOCUS

DEFINITION

AL680804

ACCESSION

AL680804

VERSION

AL680804.1

KEYWORDS

EST.

SOURCE

ORGANISM

Silurana tropicalis (western clawed frog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Silurana.

REFERENCE 1 (bases 1 to 623)

AUTHORS

Taylor, R., Ashurst, J.I., Croning, M.D.R., Zorn, A.M. and Rogers, J.

TITLE

Sanger Xenopus tropicalis EST project 2002

JOURNAL

Unpublished

COMMENT

Contact: Taylor R

Sanger Centre

BF342569 595 bp mRNA linear EST 22-NOV-2000
602013893F1 NCI-CGAP-Brn64 Homo sapiens cDNA clone IMAGE:4149623
5', mRNA sequence.

BF342569

ACCESSION

BF342569

VERSION

BF342569.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 595)

AUTHORS

NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9411 row: j column: 24

High quality sequence stop: 589.

Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: tropesanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE_ID: Tgas070b10.plcSP6
 Sequencing primer: PICSP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.

FEATURES
 source
 1..623
 /organism="Silurana tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="Tgas070b10"
 /dev_stage="gastrula (stages 10.5-13 mixed)"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-gastrula"
 /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

BASE COUNT 184 a 133 c 153 g 153 t

ORIGIN
 Query Match 86.3%; Score 16.4; DB 9; Length 623;
 Best Local Similarity 94.4%; Pred. No. 7.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AATGTCATCGTCCCGGG 19
 |||||
 Db 23 AATGTCATCGTCCCGGG 6

RESULT 12
LOCUS BG127540
DEFINITION EST473282 tomato shoot/meristem Lycopersicon esculentum cDNA clone cTOF1717 5' sequence, mRNA sequence.
ACCESSION BG127540
VERSION BG127540.1 GI:12627824
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
REFERENCE 1 (bases 1 to 682)
AUTHORS van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T., Hansen,C., Ronning,C. and Tanksley,S.
TITLE Generation of ESTs from tomato shoot/meristem tissue
JOURNAL Unpublished
COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html.

FEATURES
 source
 1..682
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cTOF1717"
 /tissue_type="shoot/meristem"
 /dev_stage="developing shoots from 4-6wks old plants"
 /lab_host="SOIR"
 /clone_lib="tomato shoot/meristem"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). tissue was immediately frozen in liquid nitrogen."

BASE COUNT 225 a 135 c 149 g 173 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 682;
Best Local Similarity 94.4%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AATGTCATCGTCCCGGG 19
 |||||
 Db 405 AATGTCATCGTCCCGGG 422

RESULT 13
LOCUS BG1758715
DEFINITION 603024016f1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194610 5', mRNA linear EST 25-SEP-2001
ACCESSION BG1758715
VERSION BG1758715.1 GI:15750280
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 768)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLNL1486 row: p column: 03
 High quality sequence start: 31
 High quality sequence stop: 752.
 Location/Qualifiers
 1..768
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5194610"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 Kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

BASE COUNT 142 a 258 c 243 g 125 t

ORIGIN
 Query Match 86.3%; Score 16.4; DB 12; Length 768;
Best Local Similarity 94.4%; Pred. No. 8.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AATGTCATCGTCCCGGG 19
 |||||
 Db 136 AATGTCATCGTCCCGAG 153

RESULT 14
LOCUS BG1754114
DEFINITION 603027673f1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197746 5', mRNA linear EST 25-SEP-2001
ACCESSION BG1754114

VERSION KEYWORDS SOURCE ORGANISM

BI754114.1 GI:15745692
EST.
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS TITLE JOURNAL COMMENT

NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L14M11495 row: b column: 19
High quality sequence stop: 757.

FEATURES source

1..799
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5197746"
/lab_host="DH103"
/clone_lib="NIH_MGC_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruher
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

BASE COUNT 135 a 281 c 261 g 122 t
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Query Match 86.3%; Score 16.4; DB 12; Length 799;
Best Local Similarity 94.4%; Pred. No. 8.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19
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Db 368 AATGTCATCGTCCCGAG 385

RESULT 15 BQ881886 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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AGENCOURT_8726413 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6340913
5', mRNA sequence.

BQ881886
BQ881886.1 GI:22273894

EST.
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 903)

NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M2538 row: b column: 18
High quality sequence stop: 699.

FEATURES source

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6340913"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH103 (phage-resistant)"
/clone_lib="NIH_MGC_47"

/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 160 a 328 c 258 g 155 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 13; Length 903;
Best Local Similarity 94.4%; Pred. No. 8.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19
|||||
Db 265 AATGTCATCGTCCCGAG 282

Search completed: August 20, 2003, 04:39:51
Job time : 47.2142 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 01:46:25 ; Search time 1.53722 Seconds
(without alignments)
5455.496 Million cell updates/sec

Title: US-09-979-558A-2
Perfect score: 19
Sequence: 1 taatgtcatgtcccgagg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	15.4	81.1	2338	4	US-09-582-337-1
3	15.4	81.1	2350	4	US-09-187-478-1
4	15.4	81.1	2350	4	US-09-292-036-1
5	14.8	77.9	99	1	US-08-427-097-12
6	14.8	77.9	99	2	US-08-878-957-12
7	14.8	77.9	170	1	US-08-419-078-5
8	14.8	77.9	170	1	US-08-419-078-6
9	14.8	77.9	170	1	US-08-726-883-5
10	14.8	77.9	170	1	US-08-726-883-6
11	14.8	77.9	300	1	US-08-419-078-4
12	14.8	77.9	300	1	US-08-726-883-4
13	14.8	77.9	384	4	US-09-389-681-451
14	14.8	77.9	384	4	US-09-620-405B-451
15	14.8	77.9	384	4	US-09-433-826B-451
16	14.8	77.9	384	4	US-09-604-287A-451
17	14.8	77.9	1322	1	US-08-419-078-1
18	14.8	77.9	1322	1	US-08-726-883-1
19	14.8	77.9	1752	1	US-08-427-097-13
20	14.8	77.9	1752	1	US-08-427-097-19
21	14.8	77.9	1752	2	US-08-878-957-13
22	14.8	77.9	1752	2	US-08-878-957-19
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24	14.4	75.8	601	4	US-09-691-861A-17
25	14.4	75.8	870	4	US-09-328-352-1475
26	14.4	75.8	1329	1	US-08-278-630A-8
27	14.4	75.8	1356	2	US-08-484-126-4

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	29	14.4	75.8	2734	4	US-09-143-571-30	Sequence 30, Appli
	30	14.4	75.8	3182	1	US-08-188-582-12	Sequence 12, Appli
	31	14.4	75.8	3182	1	US-08-646-715-12	Sequence 12, Appli
	32	14.4	75.8	9862	4	US-09-691-861A-3	Sequence 3, Appli
	33	14.4	75.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	34	14.2	74.7	881	4	US-09-370-838-288	Sequence 286, App
	35	14.2	74.7	1506	1	US-08-149-105-4	Sequence 4, Appli
	36	14.2	74.7	1506	1	US-08-317-847-4	Sequence 4, Appli
	37	14.2	74.7	1621	2	US-08-933-750C-96	Sequence 96, Appli
	38	14.2	74.7	1621	2	US-09-234-613-96	Sequence 96, Appli
	39	14.2	74.7	1794	3	US-08-123-934A-9	Sequence 9, Appli
	40	14.2	74.7	1794	3	PCT-US94-10080-9	Sequence 9, Appli
	41	14.2	74.7	8224	2	US-09-010-398-14	Sequence 14, Appli
	42	14.2	74.7	8224	3	US-09-366-260-14	Sequence 14, Appli
	43	14.2	74.7	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	44	14	73.7	3888	3	US-08-675-566-12	Sequence 12, Appli
	45	13.8	72.6	645	4	US-09-252-991A-2155	Sequence 2155, Ap

ALIGNMENTS

RESULT 1
US-09-552-322-1
; Sequence 1, Application US/09552322
; Patent No. 6436642
; GENERAL INFORMATION:
; APPLICANT: Gould-Rothberg
; APPLICANT: Rastelli
; TITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING
; TITLE OF INVENTION: DIFFERENTIAL GENE EXPRESSION
; FILE REFERENCE: 15966-548
; CURRENT APPLICATION NUMBER: US/09/552,322
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130,123
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 60/193,203
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2132
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-552-322-1

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Best Local Similarity 94.4%; Pred. No. 25;
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QY 2 AATGTCATGTCCTCCGGG 19
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DB 844 AATGTCATGTCCTCCGGG 861

RESULT 2
US-09-582-337-1/c
; Sequence 1, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
; FILE REFERENCE: JP-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 1
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; ORGANISM: Rat
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; NAME/KEY: 5'UTR
; LOCATION: (1)..(212)
; NAME/KEY: CDS
; LOCATION: (213)..(1256)
; NAME/KEY: 3'UTR
; LOCATION: (1257)..(2338)
; NAME/KEY: polyA_signal
; LOCATION: (2297)..(2302)
; US-09-582-337-1

Query Match      81.1%; Score 15.4; DB 4; Length 2338;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3
US-09-187-478-1/c
; Sequence 1, Application US/09187478
; Patent No. 6348329
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Brian F.
; TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use
; FILE REFERENCE: 08766/004001
; CURRENT APPLICATION NUMBER: US/09/187,478
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-187-478-1

Query Match      81.1%; Score 15.4; DB 4; Length 2350;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1209 ATGTCATTGTCCTCGGG 1193

RESULT 4
US-09-292-036-1/c
; Sequence 1, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIB100-1
; CURRENT APPLICATION NUMBER: US/09/292,036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-292-036-1

Query Match      81.1%; Score 15.4; DB 4; Length 2350;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATGTCATCGTCCCGGG 19
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Db      1209 ATGTCATTGTCCTCGGG 1193

RESULT 5
US-08-427-097-12
; Sequence 12, Application US/08427097
; Patent No. 5668294
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Sommers, Anne O.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,097
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 40-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-427-097-12

Query Match      77.9%; Score 14.8; DB 1; Length 99;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 6
US-08-878-957-12
; Sequence 12, Application US/08878957
; Patent No. 5965796
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Summers, Anne O.
; APPLICANT: Rugh, Clayton L.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TRANSGENIC PLANTS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/878,957
; FILING DATE: 19-JUN-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/427,097
; FILING DATE: 21-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 40-94A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-878-957-12
Query Match 77.9%; Score 14.8; DB 2; Length 99;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGG 18
DB 79 TATTGTCATCGACCCCGG 96

RESULT 7
US-08-419-078-5/c
; Sequence 5, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO

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; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Corneal Stroma
; CLONE: 046611
US-08-419-078-5
Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19
DB 134 AATGTCATCGTCCCGGG 117

RESULT 8
US-08-419-078-6/c
; Sequence 6, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 170 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ IMMEDIATE SOURCE:
/ LIBRARY: Fibroblast
/ CLONE: 054216
US-08-419-078-6
Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGG 19
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Db 134 AATGTCATCGTCCACGG 117

RESULT 9
US-08-726-883-5/c
; Sequence 5, Application US/08726883
; Patent No. 5676946
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,883
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/419,078
; FILING DATE: 10-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Fibroblast
; CLONE: 054216
US-08-726-883-6
Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGG 19
| | | | | | | | | | | | | | |
Db 134 AATGTCATCGTCCACGG 117

RESULT 10
US-08-726-883-6/c
; Sequence 6, Application US/08726883
; Patent No. 5676946
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,883
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/419,078
; FILING DATE: 10-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Fibroblast
; CLONE: 054216
US-08-726-883-6
Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGG 19
| | | | | | | | | | | | | | |
Db 134 AATGTCATCGTCCACGG 117

RESULT 11
US-08-419-078-4/c
; Sequence 4, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,883
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/419,078
; FILING DATE: 10-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Corneal Stroma
; CLONE: 046611
US-08-726-883-5
Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGG 19
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COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,078
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF0030 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Hybrid T/B Lymphoblast
CLONE: 043866
US-08-419-078-4

Query Match 77.9%; Score 14.8; DB 1; Length 300;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19
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Db 256 AATGTCATCTCCACGGG 239

RESULT 12
US-08-726-883-4/c
; Sequence 4, Application US/08726883
; Patent No. 5676946
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SELHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCITE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,883
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/419,078
; FILING DATE: 10-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555

TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Hybrid T/B Lymphoblast
CLONE: 043866
US-08-726-883-4

Query Match 77.9%; Score 14.8; DB 1; Length 300;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19
||||| ||| ||| |||
Db 256 AATGTCATCTCCACGGG 239

RESULT 13
US-09-389-681-451
; Sequence 451, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 451
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(384)
; OTHER INFORMATION: n = A,T,C or G
US-09-389-681-451

Query Match 77.9%; Score 14.8; DB 4; Length 384;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19
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Db 171 AATGTCATCTCCACGGG 188

RESULT 14
US-09-620-405B-451
; Sequence 451, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20

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/ NUMBER OF SEQ ID NOS: 495
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 451
/ LENGTH: 384
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)...(384)
/ OTHER INFORMATION: n = A,T,C or G
US-09-620-405B-451
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Query Match      77.9%; Score 14.8; DB 4; Length 384;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
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Db      171 AATGTCATCTCCACGGG 188
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RESULT 15
US-09-433-826B-451
/ Sequence 451, Application US/09433826B
/ Patent No. 6579573
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Yuqui
/ APPLICANT: Dillon, Devin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Harlocker, Susan L.
/ TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
/ TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.470C4
/ CURRENT APPLICATION NUMBER: US/09/433,826B
/ CURRENT FILING DATE: 1999-11-03
/ NUMBER OF SEQ ID NOS: 474
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 451
/ LENGTH: 384
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)...(384)
/ OTHER INFORMATION: n = A,T,C or G
US-09-433-826B-451
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Query Match      77.9%; Score 14.8; DB 4; Length 384;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
        ||||| ||||| |||||
Db      171 AATGTCATCTCCACGGG 188
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Search completed: August 20, 2003, 04:42:14
Job time : 5.53722 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 03:41:01 ; Search time 18.9385 Seconds
(without alignments)
2255.463 Million cell updates/sec

Title: US-09-979-558A-2

Perfect score: 19

Sequence: 1 taatgtcatgtcccgagg 19

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	16.4	86.3	1882	14	US-10-102-806-301
2	16.4	86.3	1926	9	US-09-764-853-238
3	16.4	86.3	1987	9	US-09-818-143-20
4	16.4	86.3	1989	11	US-09-946-374-76
5	16.4	86.3	1989	12	US-10-015-387A-76
6	16.4	86.3	1989	12	US-10-006-130A-76
7	16.4	86.3	1989	12	US-10-006-172A-76
8	16.4	86.3	1989	14	US-10-006-856A-76
9	16.4	86.3	1989	14	US-10-006-818A-76
10	16.4	86.3	1989	14	US-10-015-393A-76
11	16.4	86.3	1989	14	US-10-015-869A-76
12	16.4	86.3	1989	14	US-10-012-121A-76
13	16.4	86.3	1989	14	US-10-006-116A-76
14	16.4	86.3	1989	14	US-10-006-117A-76
15	16.4	86.3	1989	14	US-10-017-527A-76
16	16.4	86.3	1989	14	US-10-013-913A-76

17	16.4	86.3	1989	14	US-10-007-194A-76	Sequence 76, Appl
18	16.4	86.3	1989	14	US-10-013-430A-76	Sequence 76, Appl
19	16.4	86.3	1989	14	US-10-011-671A-76	Sequence 76, Appl
20	16.4	86.3	1989	14	US-10-012-755A-76	Sequence 76, Appl
21	16.4	86.3	1989	14	US-10-015-386A-76	Sequence 76, Appl
22	16.4	86.3	1989	14	US-10-011-692A-76	Sequence 76, Appl
23	16.4	86.3	1989	14	US-10-006-768A-76	Sequence 76, Appl
24	16.4	86.3	1989	14	US-10-017-610A-76	Sequence 76, Appl
25	16.4	86.3	1989	14	US-10-006-063A-76	Sequence 76, Appl
26	16.4	86.3	1989	14	US-10-020-063A-76	Sequence 76, Appl
27	16.4	86.3	1989	14	US-10-015-391A-76	Sequence 76, Appl
28	16.4	86.3	1989	14	US-10-017-407A-76	Sequence 76, Appl
29	16.4	86.3	1989	15	US-10-006-041A-76	Sequence 76, Appl
30	16.4	86.3	1989	15	US-10-011-833A-76	Sequence 76, Appl
31	16.4	86.3	1989	15	US-10-013-822A-76	Sequence 76, Appl
32	16.4	86.3	2040	14	US-10-198-846-10830	Sequence 10830, A
33	16.4	86.3	2132	14	US-10-137-473-1	Sequence 1, Appl
34	16.4	86.3	3152	14	US-10-091-438-274	Sequence 274, App
35	15.8	83.2	268	10	US-09-960-352-14693	Sequence 14693, A
36	15.8	83.2	286	10	US-09-960-352-2142	Sequence 2142, Ap
37	15.8	83.2	286	10	US-09-960-352-3787	Sequence 3787, Ap
38	15.8	83.2	286	10	US-09-960-352-9010	Sequence 9010, Ap
39	15.8	83.2	286	10	US-09-960-352-10176	Sequence 10176, A
40	15.8	83.2	286	10	US-09-960-352-11136	Sequence 11126, A
41	15.8	83.2	286	10	US-09-960-352-13502	Sequence 13502, A
42	15.8	83.2	286	10	US-09-960-352-13526	Sequence 13526, A
43	15.8	83.2	287	10	US-09-960-352-1636	Sequence 1636, Ap
44	15.8	83.2	288	10	US-09-960-352-11141	Sequence 11141, A
45	15.8	83.2	290	10	US-09-960-352-10635	Sequence 10635, A

ALIGNMENTS

RESULT 1

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US-10-102-806-301
; Sequence 301, Application US/10102806
; Publication No. US2003005442A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103PIC1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 301
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (223)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1840)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1849)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-301
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Query Match 86.3%; Score 16.4; DB 14; Length 1882;
Best Local Similarity 94.4%; Pred. No. 53;

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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGGG 19
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Db 529 AATGTCATCGTCCCGAG 546

RESULT 2
US-09-764-853-238
; Sequence 238, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-238

Query Match 86.3%; Score 16.4; DB 9; Length 1926;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGGG 19
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Db 573 AATGTCATCGTCCCGAG 590

RESULT 3
US-09-818-143-20
; Sequence 20, Application US/09818143
; Patent No. US20020019000A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES
; FILE REFERENCE: PB-0004 CIP
; CURRENT APPLICATION NUMBER: US/09/818,143
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 3948614CBI
US-09-818-143-20

Query Match 86.3%; Score 16.4; DB 9; Length 1987;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGGG 19
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Db 716 AATGTCATCGTCCCGAG 733

RESULT 4
US-09-946-374-76
; Sequence 76, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
```

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
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; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; Prior Filing Date: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-387A-76

Query Match      86.3%; Score 16.4; DB 12; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
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RESULT 6
US-10-006-130A-76
; Sequence 76, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; Prior Filing Date: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-130A-76

Query Match      86.3%; Score 16.4; DB 12; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
      |||||
Db      715 AATGTCATCGTCCCGAG 732

RESULT 7
US-10-006-172A-76
; Sequence 76, Application US/10006172A
; Publication No. US2003015300A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; Prior Filing Date: 2002-03-19
; Prior Application Number: 60/098716
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098723
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098749
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098750
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098803
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098821
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098843
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/099536
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099596
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; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099741
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099754
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099763
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099792
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099808
; Prior Filing Date: 1998-09-10
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; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099816
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/100385
; Prior Filing Date: 1998-09-15
; Prior Application Number: 60/100388
; Prior Filing Date: 1998-09-15
; Prior Application Number: 60/100390
; Prior Filing Date: 1998-09-15
; Prior Application Number: 60/100584
; Prior Filing Date: 1998-09-16
; Prior Application Number: 60/100627
; Prior Filing Date: 1998-09-16
; Prior Application Number: 60/100661
; Prior Filing Date: 1998-09-16
; Prior Application Number: 60/100662
; Prior Filing Date: 1998-09-16

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;; PRIOR FILING DATE: 1998-09-17
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;; PRIOR FILING DATE: 1998-09-17
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;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102965

;; PRIOR FILING DATE: 1998-10-02
;; PRIOR APPLICATION NUMBER: 60/103258
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103314
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;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105882
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 12; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATGTCCTCCGGG 19
|||||

Db 715 AATGTCATGTCCTCCGGG 732
|||||

RESULT 8

US-10-006-856A-76
; Sequence 76, Application US/10006856A
; Publication No. US2003004841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

```

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; PRIORITY FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-856A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
      |||||
Db      715 AATGTCATCGTCCCGAG 732

RESULT 9
US-10-006-818A-76
; Sequence 76, Application US/10006818A
; Publication No. US20030054408A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; PRIORITY FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-818A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
      |||||
Db      715 AATGTCATCGTCCCGAG 732

RESULT 10
US-10-015-393A-76
; Sequence 76, Application US/10015393A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; PRIORITY FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
      |||||
Db      715 AATGTCATCGTCCCGAG 732

RESULT 11
US-10-015-869A-76
; Sequence 76, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; PRIORITY FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
      |||||
Db      715 AATGTCATCGTCCCGAG 732

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QY      2 AATGTCATCGTCCCGGG 19
Db      715 AATGTCATCGTCCCGAG 732

RESULT 12
US-10-012-121A-76
; Sequence 76, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pionl, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012.121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-121A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
Db      715 AATGTCATCGTCCCGAG 732

RESULT 13
US-10-006-116A-76
; Sequence 76, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pionl, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C15
; CURRENT APPLICATION NUMBER: US/10/006.116A
; CURRENT FILING DATE: 2001-12-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-116A-76

; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
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; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
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;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCGGG 19
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Db 715 AATGTCATCGTCCCGAG 732

RESULT 14

US-10-006-117A-76
; Sequence 76, Application US/10006117A
; Publication NO. US20030082627A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C13
; CURRENT APPLICATION NUMBER: US/10/006,117A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-117A-76

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Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
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Db      715 AATGTCATCGTCCCGAG 732

RESULT 15
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P28301C63
; CURRENT APPLICATION NUMBER: US/10/017,527A
; CURRENT FILING DATE: 2001-12-13
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; PRIOR APPLICATION NUMBER: 60/098723
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; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
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65 PRIOR FILING DATE: 1998-10-28

Search completed: August 20, 2003, 06:42:14
Job time : 19.9385 secs

Query Match 86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 AATGTCATCGTCCCGG 19
Db 715 AATGTCATCGTCCCGG 732
|||||